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OM protein - protein search, using sw model

Run on: November 12, 2003, 11:07:32 ; Search time 21 Seconds
(without alignments)
62.459 Million cell updates/sec

Title: US-09-446-543A-5
Perfect score: 1.72
Sequence: 1 SRAHQSMETPTDINPANYAGRGIRPVGRF 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310358 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA.*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCUTS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	100.0	31	3	US-09-105-678A-7
2	172	100.0	31	3	US-09-105-678A-31
3	172	100.0	31	3	US-08-776-971-5
4	172	100.0	31	3	US-08-776-971-37
5	172	100.0	31	3	US-08-421-208-7
6	172	100.0	31	3	US-09-421-208-31
7	172	100.0	31	4	US-09-560-915-13
8	172	100.0	32	3	US-09-105-678A-32
9	172	100.0	32	3	US-08-776-971-6
10	172	100.0	32	3	US-09-421-208-32
11	172	100.0	33	3	US-09-105-678A-33
12	172	100.0	33	3	US-08-776-971-7
13	172	100.0	33	3	US-09-421-208-33
14	172	100.0	98	3	US-08-776-971-1
15	172	100.0	98	3	US-08-776-971-44
16	172	100.0	98	3	US-08-776-971-122
17	172	100.0	98	3	US-08-776-971-131
18	172	100.0	98	3	US-08-776-971-136
19	168	97.7	98	3	US-08-776-971-115
20	168	97.7	98	3	US-08-776-971-117
21	163	94.8	31	3	US-09-105-678A-8
22	163	94.8	31	3	US-09-105-678A-37
23	163	94.8	31	3	US-09-172-353-4
24	163	94.8	31	3	US-08-776-971-47
25	163	94.8	31	3	US-09-421-208-8
26	163	94.8	31	3	US-09-421-208-37
27	163	94.8	31	4	US-09-560-915-14

28	163	94.8	31	4	US-09-799-955-4	Sequence 4, Appli
29	163	94.8	32	3	US-09-105-678A-38	Sequence 38, Appli
30	163	94.8	32	3	US-08-776-971-48	Sequence 48, Appli
31	163	94.8	32	3	US-09-421-208-38	Sequence 38, Appli
32	163	94.8	33	3	US-09-105-678A-39	Sequence 39, App
33	163	94.8	33	3	US-08-776-971-49	Sequence 49, Appli
34	163	94.8	33	3	US-09-421-208-39	Sequence 39, Appli
35	163	94.8	83	3	US-08-776-971-45	Sequence 45, Appli
36	163	94.8	83	3	US-08-776-971-124	Sequence 124, App
37	163	94.8	83	3	US-08-776-971-137	Sequence 137, App
38	161	93.6	29	3	US-09-105-678A-29	Sequence 29, Appli
39	161	93.6	29	3	US-08-776-971-3	Sequence 3, Appli
40	161	93.6	29	3	US-09-421-208-29	Sequence 29, Appli
41	158	91.9	31	3	US-09-105-678A-9	Sequence 9, Appli
42	158	91.9	31	3	US-09-105-678A-43	Sequence 43, Appli
43	158	91.9	31	3	US-08-776-971-61	Sequence 61, Appli
44	158	91.9	31	3	US-09-421-208-9	Sequence 9, Appli
45	158	91.9	31	3	US-09-421-208-43	Sequence 43, Appli

ALIGNMENTS

RESULT 1
US-09-105-678A-7
Sequence 7, Application US/09105678A
Patent No. 6103882

GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19F2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/105.678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: Peptide
US-09-105-678A-7

Query Match 100.0%; Score 172; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SRAHQSMETPTDINPANYAGRGIRPVGRF 31

STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASCUEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776.971B
FILING DATE: 06-Feb-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-JUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-08-776-971-97
Query Match 100.0%; Score 172; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SRAHSHMEIRTPDINPAWYAGRGIRPVGRF 31
DB 1 SRAHSHMEIRTPDINPAWYAGRGIRPVGRF 31
RESULT 5
US-09-421-208-7
Sequence 31, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421.208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/105.678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-421-208-7
Query Match 100.0%; Score 172; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SRAHSHMEIRTPDINPAWYAGRGIRPVGRF 31
DB 1 SRAHSHMEIRTPDINPAWYAGRGIRPVGRF 31
RESULT 6
US-09-421-208-31
Sequence 31, Application US/09421208
Patent No. 6258561
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/421.208
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/105,678
FILING DATE: 26-JUN-1998
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

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; MOLECULE TYPE: peptide
US-09-421-208-31

Query Match      100.0%; Score 172; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSMSEIRTPDINPAWYAGRGIRPVGRF 31
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DB 1 SRAHQSMSEIRTPDINPAWYAGRGIRPVGRF 31
    |||||

RESULT 7
US-09-560-915-13
; Sequence 13, Application US/09560915
; Patent No. 6383764
; GENERAL INFORMATION:
; APPLICANT: Cive, Li, Olvier
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Therapeutic Compositions and Methods
; TITLE OF INVENTION: Relating to Prolactin Releasing Peptide (PRP)
; FILE REFERENCE: P-C 3534
; CURRENT APPLICATION NUMBER: US/59/560-915
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 31
; TYPE: PRP
; ORGANISM: Bos taurus
US-09-560-915-13

Query Match      100.0%; Score 172; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSMSEIRTPDINPAWYAGRGIRPVGRF 31
    |||||
DB 1 SRAHQSMSEIRTPDINPAWYAGRGIRPVGRF 31
    |||||

RESULT 8
US-09-105-678A-32
; Sequence 32, Application US/09105678A
; Patent No. 6103882
; GENERAL INFORMATION:
; APPLICANT: Suenaga, Masato
; APPLICANT: Moriya, Takeo
; APPLICANT: Tanaka, Yoko
; APPLICANT: Nishimura, Osamu
; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,678A
; FILING DATE: 26-JUN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 172118/1997
; FILING DATE: 27-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.
; REGISTRATION NUMBER: 27,026

Query Match      100.0%; Score 172; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSMSEIRTPDINPAWYAGRGIRPVGRF 31
    |||||
DB 1 SRAHQSMSEIRTPDINPAWYAGRGIRPVGRF 31
    |||||

REFERENCE/DOCKET NUMBER: 48466-342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-105-678A-32

Query Match      100.0%; Score 172; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSMSEIRTPDINPAWYAGRGIRPVGRF 31
    |||||
DB 1 SRAHQSMSEIRTPDINPAWYAGRGIRPVGRF 31
    |||||

RESULT 9
US-09-776-971-6
; Sequence 6, Application US/08776971B
; Patent No. 6228984
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Habata, Yugo
; APPLICANT: Kawamata, Yuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Kitada, Chieko
; TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,971B
; FILING DATE: 06-Feb-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/03821
; FILING DATE: 28-DEC-1996
; APPLICATION NUMBER: JP 7/343371
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: JP 8/59419
; FILING DATE: 15-MAR-1996
; APPLICATION NUMBER: JP 8/211805
; FILING DATE: 12-AUG-1996
; APPLICATION NUMBER: JP 8/246573
; FILING DATE: 18-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Conlin, David G.
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 47176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 6,
US-08-776-971-5

Query Match 100.0% Score 172; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHSHMEIRTPDINPAWYAGRGIRPVGRF 31
|||||
Db 1 SRAHSHMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 10
US-09-421-208-32

Sequence 32, Application US/09421208
Patent No. 6258561

GENERAL INFORMATION:

APPLICANT: Suenaga, Masato

APPLICANT: Moriya, Takeo

APPLICANT: Tanaka, Yoko

APPLICANT: Nishimura, Osamu

TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0. Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09421208

FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Corlin, David G.

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 48466-342

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-421-208-32

Query Match 100.0% Score 172; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SRAHSHMEIRTPDINPAWYAGRGIRPVGRF 31
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Db 1 SRAHSHMEIRTPDINPAWYAGRGIRPVGRF 31

Seq ID NO. 3
AC NO: US-08-776-971
Pat NO: 6228984; Database: Signed_Patents_AA

Db 1 SRAHNSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 2
US-09-105-678A-31
Sequence 31, Application US/09105678A
Patent No. 6103882
GENERAL INFORMATION:
APPLICANT: Suenaga, Masato
APPLICANT: Moriya, Takeo
APPLICANT: Tanaka, Yoko
APPLICANT: Nishimura, Osamu
TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,678A
FILING DATE: 26-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 172118/1997
FILING DATE: 27-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,028
REFERENCE/DOCKET NUMBER: 48466-342
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: linear
MOLECULE TYPE: peptide
US-09-105-678A-31

Query Match 100.0%; Score 172; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHNSMEIRTPDINPAWYAGRGIRPVGRF 31
Db 1 SRAHNSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 3
US-08-776-971-5
Sequence 5, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fuji, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-Feb-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-08-776-971-5

Query Match 100.0%; Score 172; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHNSMEIRTPDINPAWYAGRGIRPVGRF 31
Db 1 SRAHNSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 4
US-08-776-971-97
Sequence 97, Application US/08776971B
Patent No. 6228984
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Habata, Yugo
Kawamata, Yuji
Hosoya, Masaki
Fuji, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 11:04:47 ; Search time 41 Seconds
(without alignments)
120.013 Million cell updates/sec

Title: US-09-446-543A-5
Perfect score: 172
Sequence: 1 SPAHCHSNEIRTPDINPAKACGIRPVGRF 31

Scoring table: BLOSUM62
Gapop 10.0 Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 3
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_19Jun03.*

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- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	100.0	31	AAW31371	Sovine G protein-c
2	172	100.0	31	AAW97218	Bovine pituitary-d
3	172	100.0	31	AAW87613	Bovine 19P2 ligand
4	172	100.0	31	AAW95188	Bovine pituitary-d
5	172	100.0	31	AAW10347	Bovine oxytocin se
6	172	100.0	31	AAW49290	19P2 ligand peptid
7	172	100.0	31	AAW49298	19P2 ligand peptid
8	172	100.0	31	AAW62516	Bovine CRH releasi
9	172	100.0	31	AAE26399	Bovine PrRP-31 pep

10	172	100.0	31	ABU60825	Peptide production
11	172	100.0	31	ABU60831	Peptide production
12	172	100.0	32	AAW31372	Sovine G protein-c
13	172	100.0	32	AAW95189	Bovine pituitary-d
14	172	100.0	32	AAW30148	Bovine oxytocin se
15	172	100.0	32	AAW62517	Bovine CRH releasi
16	172	100.0	32	ABU60832	Peptide production
17	172	100.0	33	AAW31373	Sovine G protein-c
18	172	100.0	33	AAW95190	Bovine pituitary-d
19	172	100.0	33	AAW10349	Bovine oxytocin se
20	172	100.0	33	AAW49297	19P2 ligand peptid
21	172	100.0	33	AAW62518	Bovine CRH releasi
22	172	100.0	33	ABU60833	Peptide production
23	172	100.0	33	AAW31382	Bovine genome deri
24	172	100.0	38	AAW31388	Bovine G protein-c
25	172	100.0	38	AAW97224	Bovine genome deri
26	172	100.0	38	AAW97217	Bovine pituitary-d
27	172	100.0	38	AAW95187	Bovine genome deri
28	172	100.0	38	AAW10346	Bovine oxytocin se
29	172	100.0	38	AAW10353	Bovine CRH releasi
30	172	100.0	38	AAW62515	Bovine CRH releasi
31	172	100.0	38	AAW62522	Proactin releasin
32	166	96.5	31	AAW90995	Proactin releasin
33	164	95.3	31	AAW73370	bPrRP31 peptide, u
34	163	94.8	31	AAW31384	Rat type G protein
35	163	94.8	31	AAW97233	Rat type ligand po
36	163	94.8	31	AAW87614	Rat 19P2 ligand
37	163	94.8	31	AAW95173	Murine pituitary-d
38	163	94.8	31	AAW95174	Murine pituitary-d
39	163	94.8	31	AAW10355	Rat oxytocin secre
40	163	94.8	31	AAW87604	Rat prolactin rele
41	163	94.8	31	AAW49292	19P2 ligand peptid
42	163	94.8	31	AAW62524	Rat CRH releasin
43	163	94.8	31	AAW90993	Proactin releasin
44	163	94.8	31	AAW62600	Rat PrRP-31 peptid
45	163	94.8	31	ABU60826	Peptide production

ALIGNMENTS

RESULT:

AAW31371

ID AAW31371 standard; Peptide; 31 AA.

XX AAW31371:

XX (first entry)

DE Bovine G protein-coupled receptor; ligand peptide fragment 1.

XX G protein-coupled receptor; ligand binding, pharmacological

XX modulator; pituitary; central nervous system; pancreas; prophyllactic;

XX therapeutic agent.

CS Bos taurus.

XX MO3724436-A2.

XX 10-JUL-1997.

XX 26-DEC-1996; 96WO-JP03821.

XX 18-SEP-1996; 96JP-0246573.

XX 28-DEC-1995; 95JP-0343371.

XX 15-MAR-1996; 96JP-0059419.

XX 12-AUG-1996; 96JP-0211805.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;

XX Kawamata Y, Kitada C,

XX

DR WPI: 1997-363672/33.
 DR N-PSDB; AAV02394.
 XX
 PT Ligand peptide for G protein-coupled receptor - acts by modulating
 PT function in the central nervous system, pancreas and pituitary gland
 XX
 PS Claim 2; Page 160; 258pp; English.
 XX
 CC This sequence represents a peptide fragment of a novel bovine pituitary
 CC derived ligand corresponding to amino acid residues 23 to 53 of the
 CC sequence in AAW1368 and is used in an assay to monitor ligand binding
 CC to the G protein-coupled receptor protein. Pharmaceutical compositions
 CC containing this ligand may be used as a pituitary function modulator, a
 CC central nervous system modulator or a pancreatic function modulator.
 CC This ligand could have specific applications as a prophylactic or
 CC therapeutic agent for dementia, depression, hyperkinetic syndrome,
 CC disturbance of consciousness, anxiety syndrome, schizophrenia, trauma,
 CC growth hormone secretory disease, hyper- and polyphagia,
 CC hypercholesterolemia, hyperglycaemia, hyperlipidaemia,
 CC hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease,
 CC Turner's syndrome, neurosis, rheumatoid arthritis, spinal injury,
 CC transient brain ischaemia, amyotrophic lateral sclerosis, acute
 CC myocardial infarction, spinocerebellar degeneration, bone fracture,
 CC trauma, atopic dermatitis, osteoporosis, asthma, epilepsy, infertility
 CC and/or oligogalactia. Assays can also be developed to screen compounds
 CC which are capable of altering the binding activity of the ligand thus
 CC affecting activation of the G protein-coupled receptor protein.
 XX
 SQ Sequence 31 AA:
 Query Match 100.0%; Score 172; DB 18; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1,1e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 2; Gaps 0;
 *QY 1 SRAPQHSMEIRTPDINPAWYAGRGIRPVGRF 31
 |||||
 Db 1 SRAPQHSMEIRTPDINPAWYAGRGIRPVGRF 31
 |||||
 RESULT 2
 AAW97218
 ID AAW97218 standard; peptide; 31 AA.
 AC AAW97218;
 XX
 DT 06-MAY-1999 (first entry)
 DE
 XX Bovine pituitary-derived ligand polypeptide fragment.
 XX
 KW Bovine pituitary-derived ligand; modulation; prolactin secretion;
 KW G protein-coupled receptor; GPCR; hypovarianism; gonocyst cacogenesis;
 KW menopausal syndrome; euthyroid; hypometabolism; lactation;
 KW pituitary adenomatosis; brain tumour; emmenopathy; autoimmune disease;
 KW prolactinoma; infertility; impotence; amenorrhea; galactorrhea;
 KW acromegaly; Chiari-Frommel syndrome; Argonz-dei Castilo syndrome;
 KW Forbes-Albright syndrome; lymphoma; Sheehan syndrome; dyszoospermia;
 KW contraceptive; placental function; chorioncarcinoma; hydatid mole;
 KW interruption mole; abortion; unthrifty fetus; abnormal saccharometabolism;
 KW abnormal lipidmetabolism; oxytocia.
 XX
 OS Bos sp.
 XX
 PN WO9859962-A1.
 XX
 PD 30-DEC-1998.
 XX
 PP 22-JUN-1998; 98WO-JP02765.
 XX
 PR 23-JUN-1997; 97JP-0165437.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fujii R, Hinuma S, Kawanata Y, Matsumoto H;
 WPI: 1997-363672/33.
 Use of G protein-coupled receptor ligands - for modulating prolactin
 secretion or placental function, ie.g. for treating menopausal
 syndrome, tumours, autoimmune disease or abnormal pregnancy
 Claim 3; Page 135; 241pp; English.
 The present sequence represents a bovine pituitary-derived ligand
 fragment. It is used in the course of the invention. The specification
 describes an agent for modulating prolactin secretion which comprises a
 ligand polypeptide or a salt, for a G protein-coupled receptor (GPCR)
 protein. The agents for promoting prolactin secretion can be used for
 treating or preventing hypovarianism, gonocyst cacogenesis, menopause,
 syndrome, euthyroid or hypometabolism. They can be used for promoting
 lactation in a domestic mammal and as an aphrodisiac. The agents for
 inhibiting prolactin secretion can be used for treating or preventing
 pituitary adenomatosis, brain tumour, emmenopathy, autoimmune disease,
 prolactinoma, infertility, impotence, amenorrhea, galactorrhea,
 acromegaly, Chiari-Frommel syndrome, Argonz-dei Castilo syndrome,
 Forbes-Albright syndrome, lymphoma, Sheehan syndrome or dyszoospermia.
 The inhibitory agents can also be used as contraceptives. The agents for
 modulating placental function can be used for treating or preventing
 chorioncarcinoma, hydatid mole, interruption mole, abortion, unthrifty fetus,
 abnormal saccharometabolism, abnormal lipidmetabolism or oxytocia.
 Query Match 100.0%; Score 172; DB 20; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1,1e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 3; Gaps 0;
 QY 1 SRAPQHSMEIRTPDINPAWYAGRGIRPVGRF 31
 |||||
 Db 1 SRAPQHSMEIRTPDINPAWYAGRGIRPVGRF 31
 |||||
 RESULT 3
 AAW87613
 ID AAW87613 standard; Peptide; 31 AA.
 AC AAW87613;
 XX
 DT 29-MAR-1999 (first entry)
 DE
 XX Bovine 19P2 ligand.
 XX
 KW 19P2 ligand; G protein coupled receptor; pituitary;
 KW prolactin releasing peptide; catule; dementia; breast cancer;
 KW therapy.
 XX
 OS Bos taurus.
 XX
 PN EP087417-A2.
 XX
 PD 30-DEC-1998.
 XX
 PF 25-JUN-1998; 98EP-0111725.
 XX
 PR 27-JUN-1997; 97JP-0172118.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Moriya T, Nishimura O, Suenaga M, Tanaka Y;
 WPI: 1999-047884/05.
 XX
 DR Producing a 19P2 pituitary G protein receptor ligand - by cleavage
 PT of a fusion protein, useful for preventing and treating dementia,
 PT breast cancer, renal failure and autoimmune disease
 XX
 PS Claim 5; Page 34; 56pp; English.

XX This is the amino acid sequence of the bovine pituitary G
 CC protein-coupled receptor ligand 19p2L. A method suitable for
 CC commercial high-level production of 19p2L comprises expressing
 CC the ligand in host cells as a recombinant fusion protein e.g. with
 CC human basic fibroblast growth factor (see RA81792-93) that has
 CC been modified to include an N-terminal cysteine residue. The
 CC ligand is released from the fusion by cyanation followed by
 CC ammonolysis. 19p2L has prolactin secretion-stimulating and (at
 CC high doses) prolactin secretion-inhibiting properties. It can be
 CC used in the treatment and prevention of various diseases including:
 CC senile dementia, cerebrovascular dementia, and dementia associated
 CC with: genealogical disorders (e.g. Alzheimer's disease, Parkinson's
 CC disease, Pick's disease, Huntington's disease), infectious diseases
 CC (e.g. Creutzfeldt-Jakob's), endocrine or metabolic disease or
 CC toxicosis (e.g. hypochloridism, vitamin B12 deficiency, alcoholism,
 CC intoxication by drugs, metal and organic compounds), tumourigenic
 CC diseases (e.g. brain tumour), traumatic diseases (e.g. chronic
 CC subarachnoid haemorrhage, and other types of dementia, depression,
 CC hyperactive child syndrome (microencephalopathy) and disturbance of
 CC consciousness. It is also useful for prevention and treatment of
 CC diseases associated with prolactin hypo and hypersecretion
 CC respectively, including: hyperprolactinaemia, pituitary adenoma,
 CC breast cancer, infertility, impotence and autoimmune disease
 CC (hypersecretion disorders), and seminal vesicle hypoplasia.
 CC osteoporosis, menopausal syndrome and renal failure (hyposecretion
 CC disorders). The 19p2 polypeptide/amide is also useful as a test
 CC reagent for study of the prolactin secretory function or as a
 CC lactagogue in mammalian farm animals.
 XX Sequence 31 AA;
 SQ

Query Match 100.0%; Score 172; DB 20; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1,1e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSMETRTDINPANYAGRGIRPVGRF 31
 |||||
 DB 1 SRAHQSMETRTDINPANYAGRGIRPVGRF 31
 |||||

RESULT 4
 AAW95188
 ID AAW95188 standard; peptide; 31 AA.
 XX
 AC AAW95188;
 CT 10-VAR-1999 (first entry)
 XX
 DE Bovine pituitary-derived ligand polypeptide fragment.
 XX
 KW Pituitary-derived ligand polypeptide; G-protein coupled orphan receptor;
 KW GPR10; UHR-1; modulator; pituitary; central nervous system; pancreas;
 KW tissue; screen; therapeutic; binding; senile dementia; ligand; murine;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; drug;
 KW Creutzfeld-Jakob disease; poisoning; schizophrenia; growth hormone;
 KW secretion; diabetes; cancer; rheumatoid arthritis; epilepsy; vasopressor;
 KW gene therapy; transgenic animal; bovine.
 XX
 OS Bos sp.
 XX
 PN WO9849295-A1.
 XX
 PD 05-NOV-1998.
 XX
 PF 27-APR-1998; 98WO-JP01923.
 XX
 PR 28-APR-1997; 97JP-0109974.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Pukusumi S, Hinuma S;
 XX
 DR WPI; 2000-452298/39.
 XX

DR WPI; 1999-009423/01.
 XX
 PT New polypeptide ligand for orphan G protein coupled receptors - used
 PT for treating disorders of central nervous system, pituitary and
 PT pancreas, and for drug screening
 XX
 PS Example 19; Page 150; 206pp; English.
 XX
 CC The invention relates to a murine pituitary-derived ligand polypeptide
 CC which is a ligand for the G-protein coupled orphan receptor designated
 CC GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing
 CC the ligand polypeptide encoding DNA are used to produce a recombinant
 CC ligand polypeptide. The ligand polypeptide, and its fragments, modulate
 CC function of the pituitary, central nervous system, pancreas and other
 CC tissues and can be used to screen for agents that modulate binding of the
 CC polypeptide to the receptor; to quantify the amount of receptor in a
 CC sample and to raise antibodies. They may also be used therapeutically,
 CC e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's
 CC diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs;
 CC diabetes; schizophrenia; disorders of growth hormone secretion; cancer;
 CC rheumatoid arthritis; epilepsy and many others, also to improve post-
 CC operative nutritional status and as vasopressor. Transgenic animals
 CC carrying the ligand polypeptide encoding DNA or its muten are used to
 CC study the function of the polypeptide-expressing genes, as models of
 CC disease, for drug screening and as source of cell lines. The ligand
 CC polypeptide DNA is used as a source of probes and primers; to identify
 CC related sequences; in receptor-binding assays; for production of Ab and
 CC antisera; in drug development; for gene therapy and to develop transgenic
 CC animals. The present sequence represents a bovine genome-derived ligand
 CC polypeptide fragment which is similar to the murine ligand-polypeptide.
 XX Sequence 31 AA;
 SQ

Query Match 100.0%; Score 172; DB 20; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1,1e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 SRAHQSMETRTDINPANYAGRGIRPVGRF 31
 |||||
 DB 1 SRAHQSMETRTDINPANYAGRGIRPVGRF 31
 |||||

RESULT 5
 AAB10347
 ID AAB10347 standard; peptide; 31 AA.
 XX
 AC AAB10347;
 CT 24-NOV-2000 (first entry)
 XX
 DE Bovine oxytocin secretion promoting peptide SEQ ID NO: 3.
 XX
 KW Bovine; oxytocin secretion promoter; G protein-coupled receptor protein;
 KW treatment; disease; pain; atonic bleeding; uterine recovery failure; cow;
 KW caesarean section; artificial fertilization; galactostasis; goat; pig;
 KW veterinary medicine; milk production.
 XX
 OS Bos taurus.
 XX
 PN WO200038704-A1.
 XX
 PD 06-JUL-2000.
 XX
 PF 22-DEC-1999; 99WO-JP07199.
 XX
 PR 25-DEC-1998; 98JP-0369585.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Matsumoto H, Kitada C, Hinuma S;
 XX
 DR WPI; 2000-452298/39.
 XX

PT Physiologically-active polypeptide recognized as ligand by G
 PT protein-coupled receptor protein, for promoting secretion of oxytocin,
 PT as drugs for diseases relating to oxytocin secretion and in veterinary
 PT medicine

XX Claim 3: Page 50; 72pp; Japanese.

XX This invention describes a novel oxytocin secretion-regulating agent
 CC which contains a ligand peptide or its salt for the G protein-coupled
 CC receptor protein. It is useful in the form of drugs for ameliorating,
 CC preventing and treating diseases relating to oxytocin secretion e.g.
 CC weak pains and atonic bleeding, before and after expulsion of placenta,
 CC uterine recovery failure, caesarean section, stoppage of artificial
 CC fertilization or galactostasis and is also applicable in veterinary
 CC medicine for promoting milk production in cow, goat and pig. This
 CC sequence represents a bovine peptide which acts as an oxytocin secretion
 CC promoter.

XX Sequence 31 AA;

Query Match 100.0%; Score 172; DB 21; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.1e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQHSMETPTDINPAWYAGRGIRPVGRF 31
 |||||
 DB 1 SRAHQHSMETPTDINPAWYAGRGIRPVGRF 31

RESULT 6

AAV49290
 ID AAV49290 standard; peptide; 31 AA.

XX AC AAV49290;

XX 22-FEB-2000 (first entry)

XX 19P2 ligand peptide fragment.

XX Monoclonal antibody; 19P2 ligand; diagnosis: prolactin secretion;
 KW pituitary; regulatory mechanism; central nervous system; pancreatic.

XX Bos sp.

XX Key Location/Qualifiers

XX Modified-site 31 /note= "C-terminal amide"

XX WO9960112-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-JP02650.

XX 21-MAY-1998; 98JP-0140293.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Matsumoto H, Kitada C, Hiruma S;

XX WPI; 2000-039381/03.

XX New monoclonal antibodies, useful in diagnosis, as drugs and in
 PT studying diseases related to ligand abnormality

XX Disclosure; Page 26; 73pp; Japanese.

XX The invention provides a monoclonal antibody which has a specific
 CC reaction with the part peptide of the C-terminal of 19P2 ligand or its
 CC derivative. The antibodies can be used in diagnosis or to treat or
 CC prevent diseases associated with abnormality in the pituitary function;
 CC regulatory mechanism (e.g. promotion of prolactin secretion), central
 CC nervous regulatory mechanism, and pancreatic function regulatory

CC mechanism. The antibody-based immunoassay can also be applied in
 CC clarifying the physiological functions of the ligand and its derivative.
 CC Sequences AAV49290-302 represent peptide fragments of the 19P2 ligand.

XX Sequence 31 AA;

Query Match 100.0%; Score 172; DB 21; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.1e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQHSMETPTDINPAWYAGRGIRPVGRF 31
 |||||

DB 1 SRAHQHSMETPTDINPAWYAGRGIRPVGRF 31

RESULT 7

AAV49298
 ID AAV49298 standard; peptide; 31 AA.

XX AC AAV49298;

XX 22-FEB-2000 (first entry)

XX 19P2 ligand peptide fragment.

XX Monoclonal antibody; 19P2 ligand; diagnosis: prolactin secretion;
 KW pituitary; regulatory mechanism; central nervous system; pancreatic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 31 /note= "C-terminal amide"

XX WO9960112-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99WO-JP02650.

XX 21-MAY-1998; 98JP-0140293.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Matsumoto H, Kitada C, Hiruma S;

XX WPI; 2000-039381/03.

XX New monoclonal antibodies, useful in diagnosis, as drugs and in
 PT studying diseases related to ligand abnormality

XX Disclosure; Page 27; 73pp; Japanese.

XX The invention provides a monoclonal antibody which has a specific
 CC reaction with the part peptide of the C-terminal of 19P2 ligand or its
 CC derivative. The antibodies can be used in diagnosis or to treat or
 CC prevent diseases associated with abnormality in the pituitary function;
 CC regulatory mechanism (e.g. promotion of prolactin secretion), central
 CC nervous regulatory mechanism, and pancreatic function regulatory
 CC mechanism. The antibody-based immunoassay can also be applied in
 CC clarifying the physiological functions of the ligand and its derivative.
 CC Sequences AAV49290-302 represent peptide fragments of the 19P2 ligand.

XX Sequence 31 AA;

Query Match 100.0%; Score 172; DB 21; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.1e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQHSMETPTDINPAWYAGRGIRPVGRF 31
 |||||

DB 1 SRAHQHSMETPTDINPAWYAGRGIRPVGRF 31

```

RESULT 8
AAG62516
ID AAG62516 standard; peptide; 31 AA.
XX AC AAG62516;
XX AC AAG62516;
D7 24-AUG-2002 (first entry)
XX DE Bovine CRH releasing protein related peptide SEQ ID NO: 3.
XX KW Cow; corticotrophin releasing hormone; CRH; G protein receptor ligand;
XX KW analgesic; hyperaldosteronism; hypercortisolemia; hypoadrenocorticism;
XX KW Addison's disease; adrenal gland hyperfunction; obesity.
XX OS Bos taurus.
XX PN WO200135994-A1.
XX PD 25-MAY-2002.
XX PF 17-NOV-2000; 2000WO-JP081119.
XX PR 18-NOV-1999; 99JP-0327900.
XX PR 26-SEP-2000; 2000JP-0297073.
XX PA TAKEI TAKEDA CHEM IND LTD.
XX PI Kitada C, Matsumoto H, Kinuma S;
XX DR WPI; 2001-355552/37.
XX PT Use of G protein receptor ligand or peptide for controlling
XX PT corticotrophin releasing hormone secretion -
XX PS Claim 3; Page 43; 90pp; Japanese.
XX CC The present sequence describes a method of controlling the secretion of
XX CC corticotrophin releasing hormone (CRH), involving the use of a G protein
XX CC receptor ligand. This can be used to control the secretion of CRH and is
XX CC useful as an analgesic or for treating, preventing or ameliorating
XX CC diseases associated with CRH secretion such as hyperaldosteronism,
XX CC hypercortisolemia, secondary or chronic hypoadrenocorticism, Addison's
XX CC disease (including boredom, nausea, pigmentation, hypogonadism, hair
XX CC loss, and hypertension), adrenal gland hypofunction and obesity. The
XX CC present sequence is a peptide used in the exemplification of the
XX CC invention.
XX SC Sequence 31 AA;
Query Match 100.0%; Score 172; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 1, 1e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SRAHQSMETPTDINPAWAGRGIRPVGRF 31
DB 1 SRAHQSMETPTDINPAWAGRGIRPVGRF 31
RESULT 9
AAE26399
ID AAE26399 standard; peptide; 31 AA.
XX AC AAE26399;
XX AC AAE26399;
D7 13-DEC-2002 (first entry)
XX DE Bovine PrRP-31 peptide.
XX KW Wakefulness; sleep disorder; prolactin releasing peptide receptor;
XX KW PrRP; GPR10; therapy; epilepsy; narcolepsy; sleep apnoea;
XX KW insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;
XX KW anticonvulsant; bovine.
XX OS Bos taurus.
XX PN WO200292829-A1.
XX PD 21-NOV-2002.
XX PF 16-MAY-2002; 2002WO-JP04735.
XX PR 17-MAY-2001; 2001JP-0147341.
XX OS Bos taurus.
XX PN US2002037533-A1.
XX PD 28-MAR-2002.
XX PF 17-AUG-2001; 2001US-0932161.
XX PR 28-APR-2000; 2000US-0560915.
XX PA (CIVE/) CIVELLI O.
XX PA (LINS/) LIN S.
XX PI Civelli O, Lin S;
XX PN WPI; 2002-403931/43.
XX PT Screening for compounds useful for promoting wakefulness or sleep, and
XX PT for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep
XX PT apnea, comprises administering a prolactin releasing peptide agonist or
XX PT antagonist -
XX PS Disclosure; Page 24; 35pp; English.
XX CC The present invention relates to a method of screening for compounds
XX CC for promoting wakefulness or sleep in a mammal. The method involves
XX CC administering a prolactin releasing peptide (PrRP) receptor (GPR10)
XX CC agonist or antagonist respectively and determining the ability of the
XX CC compound to promote wakefulness or sleep. The compounds identified
XX CC from the method are used in the therapy of epilepsy and other diseases
XX CC associated with absence seizures and in promoting wakefulness and sleep
XX CC in individuals having sleep disorders such as insomnia and narcolepsy.
XX CC PrRP receptor agonists may be used to treat common disorders which lead
XX CC to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia
XX CC and psychogenic hypersomnia. PrRP receptor antagonists are useful for
XX CC promoting sleep and for treating insomnia such as adjustment sleep
XX CC disorder and psychophysiological insomnia. The present sequence is bovine
XX CC PrRP-31 peptide.
XX SC Sequence 31 AA;
Query Match 100.0%; Score 172; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1, 1e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SRAHQSMETPTDINPAWAGRGIRPVGRF 31
DB 1 SRAHQSMETPTDINPAWAGRGIRPVGRF 31
RESULT 10
ABU60825
ID ABU60825 standard; peptide; 31 AA.
XX AC ABU60825;
XX AC ABU60825;
D7 06-MAY-2003 (first entry)
XX DE Peptide production by gene recombination associated peptide #9.
XX DE Peptide production; low-molecular peptide; KISS-1; GPR8 ligand;
XX KW gene recombination.
XX OS Bos sp.
XX PN WO200292829-A1.
XX PD 21-NOV-2002.
XX PF 16-MAY-2002; 2002WO-JP04735.
XX PR 17-MAY-2001; 2001JP-0147341.

```

XX (TAKE) TAKEDA CHEM IND LTD.
 XX Nishimura O, Suenaga M, Ito T, Kitada C;
 PI WPI: 2003-129302/12.
 XX
 XX Process for producing peptides e.g. Kiss-1 peptide and GPR8 ligand for
 PT subsequent applications by gene recombination technique through tandem
 PT repeats to provide precursor protein with specific cleavage sites .
 XX
 XX Disclosure; Page 58; 87pp; Japanese.
 XX
 XX The invention describes a method of producing a peptide comprising the
 CC excision of the N and C-terminals of a target peptide with enzymes or
 CC chemically through the attached cleavage sites repeated by ligation in a
 CC precursor protein. The method is for producing (low-molecular) peptides
 CC e.g. Kiss-1 peptide and GPR8 ligand for subsequent applications by the
 CC gene recombination technique through tandem repeats to provide
 CC a precursor protein with specific cleavage sites. With this method,
 CC peptide production can be carried out easily to provide large quantities
 CC of the required peptides. This is the amino acid sequence of a peptide
 CC associated with the peptide production method of the invention.
 XX
 XX Sequence 31 AA;
 SQ
 Query Match 100.0%; Score 172; DB 24; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.le-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SRAHQSHMEIRTPDINPANYAGRGIRPVGRF 31
 DB 1 SRAHQSHMEIRTPDINPANYAGRGIRPVGRF 31
 RESULT 12
 AAW31372
 ID AAW31372 standard; Peptide; 32 AA.
 XX
 AC AAW31372;
 DT 06-APR-1998 (first entry)
 XX
 DE Bovine G protein-coupled receptor ligand peptide fragment 2.
 XX
 KW G protein-coupled receptor; ligand binding; pharmaceutical;
 KW modulator; pituitary; central nervous system; pancreas; prophylactic;
 KW therapeutic agent.
 XX
 OS Bos taurus.
 XX
 PN WO9724436-A2.
 XX
 PD 10-JUL-1997.
 XX
 PF 26-DEC-1996; 96WO-JP03821.
 XX
 PR 18-SEP-1996; 96JP-0246573.
 PR 28-DEC-1995; 95JP-0343371.
 PR 15-MAR-1996; 96JP-0059419.
 PR 12-AUG-1996; 96JP-0211805.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;
 PI Kawamata Y, Kitada C;
 XX
 DR WPI: 1997-363672/33.
 DR N-PSGB; AAW02395.
 XX
 XX Ligand peptide for G protein-coupled receptor - acts by modulating
 PT function in the central nervous system, pancreas and pituitary gland
 XX
 PS Claim 2; Page 160-161; 258pp; English.
 XX
 CC This sequence represents a peptide fragment of a novel bovine pituitary
 CC derived ligand corresponding to amino acid residues 23 to 54 of the
 CC sequence in AAW31368 and is used in an assay to monitor ligand binding
 CC to the G protein-coupled receptor protein. Pharmaceutical compositions
 CC containing this ligand may be used as a pituitary function modulator, a
 CC central nervous system modulator or a pancreatic function modulator.
 CC This ligand could have specific applications as a prophylactic or
 CC therapeutic agent for dementia, depression, hyperkinetic syndrome,
 CC disturbance of consciousness, anxiety syndrome, schizophrenia, trauma,
 CC growth hormone secretory disease, hyper- and polyphagia,
 CC hypercholesterolaemia, hyperglycaemia, hyperlipidaemia,
 CC hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease,
 CC Turner's syndrome, neurosis, rheumatoid arthritis, spinal injury,
 CC transient brain ischaemia, amyotrophic lateral sclerosis, acute

CC precursor protein. The method is for producing (low-molecular) peptides
 CC e.g. Kiss-1 peptide and GPR8 ligand for subsequent applications by the
 CC gene recombination technique through tandem repeats to provide
 CC a precursor protein with specific cleavage sites. With this method,
 CC peptide production can be carried out easily to provide large quantities
 CC of the required peptides. This is the amino acid sequence of a peptide
 CC associated with the peptide production method of the invention.
 XX
 XX Sequence 31 AA;
 SQ
 Query Match 100.0%; Score 172; DB 24; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.le-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SRAHQSHMEIRTPDINPANYAGRGIRPVGRF 31
 DB 1 SRAHQSHMEIRTPDINPANYAGRGIRPVGRF 31
 RESULT 12
 AAW31372
 ID AAW31372 standard; Peptide; 32 AA.
 XX
 AC AAW31372;
 DT 06-APR-1998 (first entry)
 XX
 DE Bovine G protein-coupled receptor ligand peptide fragment 2.
 XX
 KW G protein-coupled receptor; ligand binding; pharmaceutical;
 KW modulator; pituitary; central nervous system; pancreas; prophylactic;
 KW therapeutic agent.
 XX
 OS Bos taurus.
 XX
 PN WO9724436-A2.
 XX
 PD 10-JUL-1997.
 XX
 PF 26-DEC-1996; 96WO-JP03821.
 XX
 PR 18-SEP-1996; 96JP-0246573.
 PR 28-DEC-1995; 95JP-0343371.
 PR 15-MAR-1996; 96JP-0059419.
 PR 12-AUG-1996; 96JP-0211805.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fujii R, Fukusumi S, Habata Y, Hinuma S, Hosoya M;
 PI Kawamata Y, Kitada C;
 XX
 DR WPI: 1997-363672/33.
 DR N-PSGB; AAW02395.
 XX
 XX Ligand peptide for G protein-coupled receptor - acts by modulating
 PT function in the central nervous system, pancreas and pituitary gland
 XX
 PS Claim 2; Page 160-161; 258pp; English.
 XX
 CC This sequence represents a peptide fragment of a novel bovine pituitary
 CC derived ligand corresponding to amino acid residues 23 to 54 of the
 CC sequence in AAW31368 and is used in an assay to monitor ligand binding
 CC to the G protein-coupled receptor protein. Pharmaceutical compositions
 CC containing this ligand may be used as a pituitary function modulator, a
 CC central nervous system modulator or a pancreatic function modulator.
 CC This ligand could have specific applications as a prophylactic or
 CC therapeutic agent for dementia, depression, hyperkinetic syndrome,
 CC disturbance of consciousness, anxiety syndrome, schizophrenia, trauma,
 CC growth hormone secretory disease, hyper- and polyphagia,
 CC hypercholesterolaemia, hyperglycaemia, hyperlipidaemia,
 CC hyperprolactinaemia, diabetes, cancer, pancreatitis, renal disease,
 CC Turner's syndrome, neurosis, rheumatoid arthritis, spinal injury,
 CC transient brain ischaemia, amyotrophic lateral sclerosis, acute

The invention relates to a murine pituitary-derived ligand polypeptide which is a ligand for the G-protein coupled orphan receptor designated GPR10 (human) or UHR-1 (rat). Cells transformed with a vector containing the ligand polypeptide encoding DNA are used to produce a recombinant ligand polypeptide. The ligand polypeptide, and its fragments, modulate function of the pituitary, central nervous system, pancreas and other tissues and can be used to screen for agents that modulate binding of the polypeptide to the receptor, to quantify the amount of receptor in a sample and to raise antibodies. They may also be used therapeutically, e.g. to treat senile dementia; Alzheimer's, Parkinson's or Huntington's diseases; Creutzfeld-Jakob disease; poisoning by heavy metals or drugs; diabetes; schizophrenia; disorders of growth hormone secretion; cancer; rheumatoid arthritis; epilepsy and many others, also to improve post-operative nutritional status and as vasopressor. Transgenic animals carrying the ligand polypeptide encoding DNA or its mutant are used to study the function of the polypeptide-expressing genes, as models of

QY 1 SRAHQHSMETPTDINPAWYAGRGIRPVGRF 31
 |||||
 Db : SRAHQHSMETPTDINPAWYAGRGIRPVGRF 31

RESULT 15

AAG62517
 ID AAG62517 standard; peptide; 32 AA.

AC AAG62517;

XX 24-AUG-2001 (first entry)

XX Bovine CRH releasing protein related peptide SEQ ID NO: 4.

DE Cow; corticotrophin releasing hormone, CRH; G protein receptor ligand;
 KW analgesic; hyperaldosteronism; hypercortisolemia; hypoadrenocorticism;
 KW Addison's disease; adrenal gland hyperfunction; obesity.

XX Bos taurus.

XX WO200135984-A1.

XX PD 25-MAY-2001.

XX 17-NOV-2000; 2000WC-JP08-19.

XX 16-NOV-1999; 99JP-0327900.

XX 26-SEP-2000; 2000JP-0297073.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Kitada C, Matsumoto H, Hinuma S;

XX WPI; 2001-355552/37.

-PT Use of G protein receptor ligand or peptide for controlling

-PT corticotropin releasing hormone secretion.

XX Disclosure; Page 64; 90pp; Japanese.

XX The present sequence describes a method of controlling the secretion of
 CC corticotrophin releasing hormone (CRH), involving the use of a G protein
 CC receptor ligand. This can be used to control the secretion of CRH and is
 CC useful as an analgesic or for treating, preventing or ameliorating
 CC diseases associated with CRH secretion such as hyperaldosteronism,
 CC hypercortisolemia, secondary or chronic hypoadrenocorticism, Addison's
 CC disease (including boredom, nausea, pigmentation, hypogonadism, hair
 CC loss, and hypotension), adrenal gland hypofunction and obesity. The
 CC present sequence is a peptide used in the exemplification of the
 CC invention.

XX SQ Sequence 32 AA;

Query Match

Best Local Similarity 100.0%; Score 172; DB 22; Length 32;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQHSMETPTDINPAWYAGRGIRPVGRF 31

Db 1 SRAHQHSMETPTDINPAWYAGRGIRPVGRF 31

Search completed: November 12, 2003, 11:08:19

Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 12, 2003, 11:08:23 ; Search time 172 Seconds
(without alignments)
163.997 Million cell updates/sec

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Perfect score: 172
Sequence: 1 SRAHQSMETPTDINPAWYAGRGIRPVGRF 31

Scoring table: BLQSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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31: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*
32: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	172	100.0	31	1 PCT-US02-24248-13 Sequence 13, Appl

2	172	100.0	31	15	US-09-105-678-7	Sequence 7, Appl
3	172	100.0	31	15	US-09-105-678-31	Sequence 31, Appl
4	172	100.0	31	18	US-09-403-639A-39	Sequence 39, Appl
5	172	100.0	31	18	US-09-403-639A-39	Sequence 39, Appl
6	172	100.0	31	18	US-09-403-639C-39	Sequence 39, Appl
7	172	100.0	31	18	US-09-446-543A-5	Sequence 5, Appl
8	172	100.0	31	19	US-09-576-290-5	Sequence 5, Appl
9	172	100.0	31	19	US-09-576-290-97	Sequence 97, Appl
10	172	100.0	31	21	US-09-116-147-5	Sequence 5, Appl
11	172	100.0	31	21	US-09-116-147-97	Sequence 97, Appl
12	172	100.0	31	23	US-09-868-885B-3	Sequence 3, Appl
13	172	100.0	31	24	US-09-932-161-13	Sequence 13, Appl
14	172	100.0	31	26	US-10-044-592-39	Sequence 39, Appl
15	172	100.0	31	26	US-10-096-777-13	Sequence 13, Appl
16	172	100.0	31	27	US-10-130-584-3	Sequence 3, Appl
17	172	100.0	32	15	US-09-105-678-32	Sequence 32, Appl
18	172	100.0	32	18	US-09-403-639A-40	Sequence 40, Appl
19	172	100.0	32	18	US-09-403-639B-40	Sequence 40, Appl
20	172	100.0	32	18	US-09-403-639C-40	Sequence 40, Appl
21	172	100.0	32	18	US-09-446-543A-6	Sequence 6, Appl
22	172	100.0	32	19	US-09-576-290-6	Sequence 6, Appl
23	172	100.0	32	21	US-09-116-147-6	Sequence 6, Appl
24	172	100.0	32	23	US-09-868-885B-4	Sequence 4, Appl
25	172	100.0	32	26	US-10-044-592-40	Sequence 40, Appl
26	172	100.0	32	27	US-10-130-584-4	Sequence 4, Appl
27	172	100.0	33	15	US-09-105-678-33	Sequence 33, Appl
28	172	100.0	33	18	US-09-403-639A-41	Sequence 41, Appl
29	172	100.0	33	18	US-09-403-639B-41	Sequence 41, Appl
30	172	100.0	33	18	US-09-403-639C-41	Sequence 41, Appl
31	172	100.0	33	18	US-09-446-543A-7	Sequence 7, Appl
32	172	100.0	33	19	US-09-576-290-7	Sequence 7, Appl
33	172	100.0	33	21	US-09-700-643A-8	Sequence 8, Appl
34	172	100.0	33	21	US-09-716-147-7	Sequence 7, Appl
35	172	100.0	33	23	US-09-968-885B-5	Sequence 5, Appl
36	172	100.0	33	26	US-10-044-592-41	Sequence 41, Appl
37	172	100.0	33	27	US-10-130-584-5	Sequence 5, Appl
38	172	100.0	98	18	US-09-403-639A-28	Sequence 28, Appl
39	172	100.0	98	18	US-09-403-639A-38	Sequence 38, Appl
40	172	100.0	98	18	US-09-403-639B-28	Sequence 28, Appl
41	172	100.0	98	18	US-09-403-639B-38	Sequence 38, Appl
42	172	100.0	98	18	US-09-403-639B-82	Sequence 82, Appl
43	172	100.0	98	18	US-09-403-639B-84	Sequence 84, Appl
44	172	100.0	98	18	US-09-403-639B-86	Sequence 86, Appl
45	172	100.0	98	18	US-09-403-639B-88	Sequence 88, Appl

ALIGNMENTS

RESULT 1
PCT-US02-24248-13
Sequence 13, Application PC/TUS0224248
GENERAL INFORMATION:
APPLICANT: Civeilli, Olivier
TITLE OF INVENTION: Screening and Therapeutic Methods For
TITLE OF INVENTION: Promoting Wakefulness and Sleep
FILE REFERENCE: P-UC 4673
CURRENT APPLICATION NUMBER: PCT/US02/24248
CURRENT FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US 09/560,915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FASTSEQ for Windows Version 4.5
SEQ ID NO 13
LENGTH: 31
TYPE: PRT
ORGANISM: Bos taurus
PCT-US02-24248-13

Query Match 100.0%; Score 172; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.1e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSHMEIRTPDINPANYAGRGIRPVGRF 31
 DB 1 SRAHQSHMEIRTPDINPANYAGRGIRPVGRF 31

RESULT 2
 US-09-105-678-7
 ; Sequence 7, Application US/09105678
 ; GENERAL INFORMATION:
 ; APPLICANT: Suenaga, Masato
 ; APPLICANT: Motiya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; APPLICANT: Nishimura, Osamu
 ; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.10
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678
 FILING DATE: 26-JUN-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Corlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

Query Match: 100.0%; Score 172; DB 15; Length 31;
 Best Local Similarity 100.0%; Pred. No. 8.1e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSHMEIRTPDINPANYAGRGIRPVGRF 31
 DB 1 SRAHQSHMEIRTPDINPANYAGRGIRPVGRF 31

RESULT 3
 US-09-105-678-31
 ; Sequence 31, Application US/09105678
 ; GENERAL INFORMATION:
 ; APPLICANT: Suenaga, Masato
 ; APPLICANT: Motiya, Takeo
 ; APPLICANT: Tanaka, Yoko
 ; APPLICANT: Nishimura, Osamu
 ; TITLE OF INVENTION: METHOD OF PRODUCING A 19P2 LIGAND
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston

STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.10
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/105,678
 FILING DATE: 26-JUN-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 172118/1997
 FILING DATE: 27-JUN-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Corlin, David G.
 REGISTRATION NUMBER: 27,026
 REFERENCE/DOCKET NUMBER: 48466-342
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-09-105-678-31
 Query Match: 100.0%; Score 172; DB 15; Length 31;
 Best Local Similarity 100.0%; Pred. No. 8.1e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSHMEIRTPDINPANYAGRGIRPVGRF 31
 DB 1 SRAHQSHMEIRTPDINPANYAGRGIRPVGRF 31

RESULT 4
 US-09-403-639A-39
 ; Sequence 39, Application US/09403639A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hinuma, Shuji
 ; APPLICANT: Fukusumi, Shoji
 ; TITLE OF INVENTION: Polypeptides, their Production and Use
 ; FILE REFERENCE: 2463USOP
 ; CURRENT APPLICATION NUMBER: US/09/403,639A
 ; CURRENT FILING DATE: 1998-04-27
 ; PRIOR APPLICATION NUMBER: PCT/JP96/01923
 ; PRIOR FILING DATE: 1998-04-27
 ; PRIOR APPLICATION NUMBER: JP 9-109974
 ; PRIOR FILING DATE: 1997-04-28
 ; NUMBER OF SEQ ID NOS: 62
 ; SOFTWARE:
 ; SEQ ID NO 39
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Bovine

US-09-403-639A-39
 Query Match: 100.0%; Score 172; DB 18; Length 31;
 Best Local Similarity 100.0%; Pred. No. 8.1e-17;
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QY 1 SRAHQSHMEIRTPDINPANYAGRGIRPVGRF 31
 DB 1 SRAHQSHMEIRTPDINPANYAGRGIRPVGRF 31

RESULT 5
 US-09-403-639B-39
 ; Sequence 39, Application US/09403639B

GENERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 APPLICANT: Fukusumi, Shoji
 TITLE OF INVENTION: Polypeptides, their Production and Use
 FILE REFERENCE: 2463USOP
 CURRENT APPLICATION NUMBER: US/09/403,639B
 PRIOR FILING DATE: 1999-10-25
 PRIOR APPLICATION NUMBER: PCT/JP98/01923
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: JP 9-109974
 PRIOR FILING DATE: 1997-04-28
 NUMBER OF SEQ ID NOS: 96
 SOFTWARE:
 SEQ ID NO 39
 LENGTH: 31
 TYPE: PRT
 ORGANISM: Bovine

US-09-403-639B-39

Query Match 100.0%; Score 172; DB 18; Length 31;
 Best Local Similarity 100.0%; Pred. No. 8.1e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 SRAHQSMEIRTPDINPAWYAGRGIRPVGRF 31
 DB 1 SRAHQSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 6

US-09-403-639C-39

Sequence 39, Application US/09403639C

GENERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 APPLICANT: Fukusumi, Shoji
 TITLE OF INVENTION: Polypeptides, their Production and Use
 FILE REFERENCE: 2463USOP
 CURRENT APPLICATION NUMBER: US/09/403,639C
 PRIOR FILING DATE: 1999-10-25
 PRIOR APPLICATION NUMBER: PCT/JP98/01923
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: JP 9-109974
 PRIOR FILING DATE: 1997-04-28
 NUMBER OF SEQ ID NOS: 96
 SOFTWARE:
 SEQ ID NO 39
 LENGTH: 31
 TYPE: PRT
 ORGANISM: Bovine

US-09-403-639C-39

Query Match 100.0%; Score 172; DB 18; Length 31;
 Best Local Similarity 100.0%; Pred. No. 8.1e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 SRAHQSMEIRTPDINPAWYAGRGIRPVGRF 31
 DB 1 SRAHQSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 7

US-09-446-543A-5

Sequence 5, Application US/09446543A

GENERAL INFORMATION:
 APPLICANT: HINUMA, Shuji
 APPLICANT: KAWAMATA, Yuji
 APPLICANT: FUJII, Ryo
 TITLE OF INVENTION: prolactin Secretion Modulator
 FILE REFERENCE: 2472USOP
 CURRENT APPLICATION NUMBER: US/09/446,543A
 CURRENT FILING DATE: 1998-12-20
 PRIOR APPLICATION NUMBER: PCT/JP98/02765
 PRIOR FILING DATE: 1998-06-22

PRIOR APPLICATION NUMBER: JP 9-165437
 PRIOR FILING DATE: 1997-06-23
 NUMBER OF SEQ ID NOS: 99
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 5
 LENGTH: 31
 TYPE: PRT
 ORGANISM: artificial
 FEATURE:
 OTHER INFORMATION: bovine fragment (23-53)
 US-09-446-543A-5

Query Match 100.0%; Score 172; DB 18; Length 31;
 Best Local Similarity 100.0%; Pred. No. 8.1e-17;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 SRAHQSMEIRTPDINPAWYAGRGIRPVGRF 31
 DB 1 SRAHQSMEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 8

US-09-576-290-5

Sequence 5, Application US/09576290

GENERAL INFORMATION:
 APPLICANT: Hinuma, Shuji
 APPLICANT: Habata, Yugo
 APPLICANT: Kawamata, Yuji
 APPLICANT: Hosoya, Masaki
 APPLICANT: Fujii, Ryo
 APPLICANT: Fukusumi, Shoji
 APPLICANT: Kitada, Chieko
 TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
 NUMBER OF SEQUENCES: 140
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
 STREET: 130 Water Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEO for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/576,290
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/776,971
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 7/34337-
 FILING DATE: 28-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 8/59419
 FILING DATE: 15-MAR-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 8/211805
 FILING DATE: 12-AUG-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 8/246573
 FILING DATE: 18-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Conlin, David G.
 REGISTRATION NUMBER: 27,025
 REFERENCE/DOCKET NUMBER: 47176
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-523-3400
 TELEFAX: 617-523-6440
 INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-576-290-5

Query Match 100.0%; Score 172; DB 19; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.1e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSMETPTDINPAWYAGRGIRPVGRF 31
DB 1 SRAHQSMETPTDINPAWYAGRGIRPVGRF 31

RESULT 9

US-09-576-290-97
Sequence 97, Application: US/0557629C

GENERAL INFORMATION:

APPLICANT: Hiruma, Shuji
APPLICANT: Habata, Yugo
APPLICANT: Kawamata, Yuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Fukusumi, Shoji
APPLICANT: Kitada, Chieko
TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/576,290
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/776,971
FILING DATE:

APPLICATION DATA: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION DATA: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION DATA: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION DATA: JP 8/246573
FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Corlin, David G.
REGISTRATION NUMBER: 27,526
REFERENCE/DOCKET NUMBER: 47,76
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 97:

SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
US-09-576-290-97

Query Match 100.0%; Score 172; DB 19; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.1e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSMETPTDINPAWYAGRGIRPVGRF 31
DB 1 SRAHQSMETPTDINPAWYAGRGIRPVGRF 31

RESULT 10

US-09-716-147-5
Sequence 5, Application US/09716.47

GENERAL INFORMATION:

APPLICANT: Hiruma, Shuji
APPLICANT: Habata, Yugo
APPLICANT: Kawamata, Yuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Fukusumi, Shoji
APPLICANT: Kitada, Chieko

TITLE OF INVENTION: POLYPROTEINS, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/716,147
FILING DATE: 17-Nov-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-FEB-1997
APPLICATION NUMBER: PCT/JP96/03821
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 8/246573
FILING DATE: 18-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Corlin, David G.
REGISTRATION NUMBER: 27,526
REFERENCE/DOCKET NUMBER: 47,76
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-716-147-5

Query Match 100.0%; Score 172; DB 21; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.1e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQHSEIIRTPDINPAWYAGRGIRPVGRF 31
DB 1 SRAHQHSEIIRTPDINPAWYAGRGIRPVGRF 31

RESULT 11
US-09-716-147-97
Sequence 97, Application US/09716147
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
Kawamata, Yuji
Hosoya, Masaki
Fujii, Ryo
Fukusumi, Shoji
Kitada, Chieko
TITLE OF INVENTION: POLYPEPTIDES, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA: US/09/716,147
FILING DATE: 17-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/776,971B
FILING DATE: 06-FEB-1997
APPLICATION NUMBER: PCT/JP96/03621
FILING DATE: 28-DEC-1996
APPLICATION NUMBER: JP 7/343371
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: JP 8/59419
FILING DATE: 15-MAR-1996
APPLICATION NUMBER: JP 8/211805
FILING DATE: 12-AUG-1996
APPLICATION NUMBER: JP 9/246573
FILING DATE: 18-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Conlin, David G.
REGISTRATION NUMBER: 27,026
REFERENCE/DOCKET NUMBER: 47176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 97:

Query Match 100.0%; Score 172; DB 21; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.1e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQHSEIIRTPDINPAWYAGRGIRPVGRF 31
DB 1 SRAHQHSEIIRTPDINPAWYAGRGIRPVGRF 31

RESULT 12
US-09-868-885B-3
Sequence 3, Application US/0986885B
GENERAL INFORMATION:
APPLICANT: Takeda Chemical Industries, Ltd.
TITLE OF INVENTION: Use of Peptide
FILE REFERENCE: 2584WOOP
CURRENT APPLICATION NUMBER: US/09/968,885B
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: JP 10-369585
PRIOR FILING DATE: 1998-12-25
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 3
LENGTH: 31
TYPE: PPT
ORGANISM: Bovine
US-09-868-885B-3

Query Match 100.0%; Score 172; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.1e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQHSEIIRTPDINPAWYAGRGIRPVGRF 31
DB 1 SRAHQHSEIIRTPDINPAWYAGRGIRPVGRF 31

RESULT 13
US-09-932-161-13
Sequence 13, Application US/09932161
GENERAL INFORMATION:
APPLICANT: Civeilli, Olivier
APPLICANT: Lin, Steven
TITLE OF INVENTION: Screening and Therapeutic Methods For
FILE REFERENCE: P-UC 4679
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 09/560,915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 31
TYPE: PPT
ORGANISM: Bos taurus
US-09-932-161-13

Query Match 100.0%; Score 172; DB 24; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.1e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQHSEIIRTPDINPAWYAGRGIRPVGRF 31
DB 1 SRAHQHSEIIRTPDINPAWYAGRGIRPVGRF 31

RESULT 14
US-10-044-592-39
Sequence 39, Application US/10044592
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Fukusumi, Shoji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/401639
PRIOR FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923

Query Match 100.0%; Score 172; DB 21; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.1e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQHSEIIRTPDINPAWYAGRGIRPVGRF 31
DB 1 SRAHQHSEIIRTPDINPAWYAGRGIRPVGRF 31

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 12, 2003, 11:09:38 ; Search time 28 Seconds
(without alignments)
190.151 Million cell updates/sec

Title: US-09-446-543a-5

Perfect score: 172

Sequence: 1 SRAHQSHWEIRTPD:NPAYAGRGIRPVGRF 31

Scoring table: BLOSUM62

Gapop: 10.0, Gapext: 0.5

Searched: 644079 seqs, 17249292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PTC_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PTCUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US08A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB IC	Description
1	172	100.0	31	9	US-09-932-161-13
2	172	100.0	31	12	US-10-096-777-13
3	172	100.0	31	14	US-10-044-592-39
4	172	100.0	32	14	US-10-044-592-40
5	172	100.0	33	14	US-10-044-592-41
6	172	100.0	98	14	US-10-044-592-28
7	172	100.0	98	14	US-10-044-592-38
8	172	100.0	98	14	US-10-044-592-82
9	172	100.0	98	14	US-10-044-592-84
10	172	100.0	98	14	US-10-044-592-86
11	172	100.0	98	14	US-10-044-592-88
12	163	94.8	31	9	US-09-932-161-14
13	163	94.8	31	12	US-10-096-777-14
14	163	94.8	31	14	US-10-044-592-4
15	163	94.8	31	14	US-10-044-592-5

16	163	94.8	70	14	US-10-044-592-90	Sequence 90, Appl
17	163	94.8	82	14	US-10-044-592-1	Sequence 1, Appl
18	163	94.8	86	14	US-10-044-592-86	Sequence 96, Appl
19	163	94.8	91	14	US-10-044-592-94	Sequence 94, Appl
20	161	93.6	29	14	US-10-044-592-26	Sequence 26, Appl
21	158	91.9	31	9	US-09-932-161-15	Sequence 15, Appl
22	158	91.9	31	12	US-10-096-777-15	Sequence 15, Appl
23	158	91.9	87	14	US-10-044-592-32	Sequence 92, Appl
24	142	82.6	25	14	US-10-044-592-28	Sequence 78, Appl
25	115	66.9	20	9	US-09-932-161-16	Sequence 16, Appl
26	115	66.9	20	12	US-10-096-777-16	Sequence 16, Appl
27	115	66.9	20	14	US-10-044-592-42	Sequence 42, Appl
28	115	66.9	21	14	US-10-044-592-43	Sequence 43, Appl
29	115	66.9	22	14	US-10-044-592-44	Sequence 44, Appl
30	111	64.5	20	9	US-09-932-161-17	Sequence 17, Appl
31	111	64.5	20	12	US-10-096-777-17	Sequence 17, Appl
32	111	64.5	20	14	US-10-044-592-6	Sequence 6, Appl
33	109	63.4	19	14	US-10-044-592-27	Sequence 27, Appl
34	109	63.4	20	9	US-09-932-161-18	Sequence 18, Appl
35	109	63.4	20	12	US-10-096-777-18	Sequence 18, Appl
36	96	55.8	40	14	US-10-044-592-80	Sequence 80, Appl
37	61	35.5	428	9	US-09-820-155-2	Sequence 2, Appl
38	57	33.1	9	14	US-10-044-592-8	Sequence 8, Appl
39	57	33.1	465	12	US-10-301-822-197	Sequence 197, App
40	56	32.6	428	9	US-09-820-155-4	Sequence 4, Appl
41	54	31.4	10	14	US-10-044-592-9	Sequence 9, Appl
42	54	31.4	209	14	US-10-108-315-30	Sequence 30, Appl
43	52	30.2	417	10	US-09-738-826-1642	Sequence 4642, Ap
44	52	30.2	3594	10	US-09-911-842-4	Sequence 4, Appl
45	52	30.2	3594	14	US-10-150-821-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-932-161-13
: Sequence 13, Application US/C9932161
: Patent No. US2002003753A1
: GENERAL INFORMATION:
: APPLICANT: Civeili, Olivier
: APPLICANT: Lin, Steven
: TITLE OF INVENTION: Screening and Therapeutic Methods For Promoting Wakefulness and Sleep
: FILE REFERENCE: P-UC 4679
: CURRENT APPLICATION NUMBER: US/09/932.161
: PRIOR FILING DATE: 2001-08-17
: PRIOR APPLICATION NUMBER: US 09/560.913
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 13
: LENGTH: 31
: TYPE: PRT
: ORGANISM: Bos taurus
US-09-932-161-13

Query Match 100.0% Score 172 DB 9: Length 31:
Best Local Similarity 100.0% Pred. No. 86-18;
Matches 31: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SRAHQSHWEIRTPDINPAWYAGRGIRPVGRF 31
|||||

Db 1 SRAHQSHWEIRTPDINPAWYAGRGIRPVGRF 31
|||||

RESULT 2

US-10-096-777-13
: Sequence 13, Application US/10096777
: Publication No. US20030171270A1
: GENERAL INFORMATION:
: APPLICANT: Civeili, Olivier
: APPLICANT: Lin, Steven

;; TITLE OF INVENTION: Therapeutic Compositions and Methods
;; FILE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP);
;; FILE REFERENCE: PUC 3534

;; CURRENT APPLICATION NUMBER: US/10/096,777

;; CURRENT FILING DATE: 2002-03-12

;; PRIOR APPLICATION NUMBER: US/09/560,915

;; PRIOR FILING DATE: 2000-04-28

;; NUMBER OF SEQ ID NOS: 24

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 13

;; LENGTH: 31

;; TYPE: PRT

;; ORGANISM: Bos taurus

US-10-096-777-13

Query Match 100.0%; Score 172; DB 12; Length 31;

Best Local Similarity 100.0%; Pred. No. 8e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSMSEIRTPDINPAWYAGRGIRPVGRF 31

DB 1 SRAHQSMSEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 3

US-10-044-592-39

;; Sequence 39, Application US/10044592

;; Publication No. US20020143152A1

;; GENERAL INFORMATION:

;; APPLICANT: Hinuma, Shuji

;; TITLE OF INVENTION: Polypeptides, their Production and Use

;; FILE REFERENCE: 2463US2P

;; CURRENT APPLICATION NUMBER: US/10/044,592

;; PRIOR FILING DATE: 2002-01-10

;; PRIOR APPLICATION NUMBER: US 09/403639

;; PRIOR FILING DATE: 1999-25-10

;; PRIOR APPLICATION NUMBER: PCT/JP98/01923

;; PRIOR FILING DATE: 1998-04-27

;; PRIOR APPLICATION NUMBER: JP 9-103974

;; PRIOR FILING DATE: 1997-04-28

;; NUMBER OF SEQ ID NOS: 96

;; SOFTWARE:

;; SEQ ID NO 39

;; LENGTH: 31

;; TYPE: PRT

;; ORGANISM: Bovine

US-10-044-592-39

Query Match 100.0%; Score 172; DB 14; Length 31;

Best Local Similarity 100.0%; Pred. No. 8e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSMSEIRTPDINPAWYAGRGIRPVGRF 31

DB 1 SRAHQSMSEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 4

US-10-044-592-40

;; Sequence 40, Application US/10044592

;; Publication No. US20020143152A1

;; GENERAL INFORMATION:

;; APPLICANT: Hinuma, Shuji

;; TITLE OF INVENTION: Polypeptides, their Production and Use

;; FILE REFERENCE: 2463US2P

;; CURRENT APPLICATION NUMBER: US/10/044,592

;; PRIOR FILING DATE: 2002-01-10

;; PRIOR APPLICATION NUMBER: US 09/403639

;; PRIOR FILING DATE: 1999-25-10

;; PRIOR APPLICATION NUMBER: PCT/JP98/01923

;; PRIOR FILING DATE: 1998-04-27

;; NUMBER OF SEQ ID NOS: 96

;; SOFTWARE:

;; SEQ ID NO 28

;; PRIOR APPLICATION NUMBER: JP 9-103974

;; PRIOR FILING DATE: 1997-04-28

;; NUMBER OF SEQ ID NOS: 96

;; SOFTWARE:

;; SEQ ID NO 40

;; LENGTH: 32

;; TYPE: PRT

;; ORGANISM: Bovine

US-10-044-592-40

Query Match 100.0%; Score 172; DB 14; Length 32;

Best Local Similarity 100.0%; Pred. No. 8.2e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSMSEIRTPDINPAWYAGRGIRPVGRF 31

DB 1 SRAHQSMSEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 5

US-10-044-592-41

;; Sequence 41, Application US/10044592

;; Publication No. US20020143152A1

;; GENERAL INFORMATION:

;; APPLICANT: Hinuma, Shuji

;; TITLE OF INVENTION: Polypeptides, their Production and Use

;; FILE REFERENCE: 2463US2P

;; CURRENT APPLICATION NUMBER: US/10/044,592

;; PRIOR FILING DATE: 2002-01-10

;; PRIOR APPLICATION NUMBER: US 09/403639

;; PRIOR FILING DATE: 1999-25-10

;; PRIOR APPLICATION NUMBER: PCT/JP98/01923

;; PRIOR FILING DATE: 1998-04-27

;; PRIOR APPLICATION NUMBER: JP 9-103974

;; PRIOR FILING DATE: 1997-04-28

;; NUMBER OF SEQ ID NOS: 96

;; SOFTWARE:

;; SEQ ID NO 41

;; LENGTH: 33

;; TYPE: PRT

;; ORGANISM: Bovine

US-10-044-592-41

Query Match 100.0%; Score 172; DB 14; Length 33;

Best Local Similarity 100.0%; Pred. No. 8.5e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSMSEIRTPDINPAWYAGRGIRPVGRF 31

DB 1 SRAHQSMSEIRTPDINPAWYAGRGIRPVGRF 31

RESULT 6

US-10-044-592-28

;; Sequence 28, Application US/10044592

;; Publication No. US20020143152A1

;; GENERAL INFORMATION:

;; APPLICANT: Hinuma, Shuji

;; TITLE OF INVENTION: Polypeptides, their Production and Use

;; FILE REFERENCE: 2463US2P

;; CURRENT APPLICATION NUMBER: US/10/044,592

;; PRIOR FILING DATE: 2002-01-10

;; PRIOR APPLICATION NUMBER: US 09/403639

;; PRIOR FILING DATE: 1999-25-10

;; PRIOR APPLICATION NUMBER: PCT/JP98/01923

;; PRIOR FILING DATE: 1998-04-27

;; PRIOR APPLICATION NUMBER: JP 9-103974

;; PRIOR FILING DATE: 1997-04-28

;; NUMBER OF SEQ ID NOS: 96

;; SOFTWARE:

;; SEQ ID NO 28

Query Match
Best Local Similarity 100.0%; Score 172; DB 14; Length 98;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-044-592-86
Query Match
Best Local Similarity 100.0%; Score 172; DB 14; Length 98;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSHMEIRTPDINPAWYAGRGIRPVGRF 31
DB 23 SRAHQSHMEIRTPDINPAWYAGRGIRPVGRF 53

RESULT 7
US-10-044-592-86
Sequence 38, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP99/01923
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: JP 9-109974
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 38
LENGTH: 98
TYPE: PRT
ORGANISM: Bovine
US-10-044-592-86

Query Match
Best Local Similarity 100.0%; Score 172; DB 14; Length 98;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSHMEIRTPDINPAWYAGRGIRPVGRF 31
DB 23 SRAHQSHMEIRTPDINPAWYAGRGIRPVGRF 53

RESULT 8
US-10-044-592-82
Sequence 82, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: JP 9-109974
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 82
LENGTH: 98
TYPE: PRT
ORGANISM: Bovine
US-10-044-592-82

Query Match
Best Local Similarity 100.0%; Score 172; DB 14; Length 98;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSHMEIRTPDINPAWYAGRGIRPVGRF 31
DB 23 SRAHQSHMEIRTPDINPAWYAGRGIRPVGRF 53

RESULT 9
US-10-044-592-84
Sequence 84, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: JP 9-109974
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 84
LENGTH: 98
TYPE: PRT
ORGANISM: Bovine
US-10-044-592-84

Query Match
Best Local Similarity 100.0%; Score 172; DB 14; Length 98;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSHMEIRTPDINPAWYAGRGIRPVGRF 31
DB 23 SRAHQSHMEIRTPDINPAWYAGRGIRPVGRF 53

RESULT 10
US-10-044-592-86
Sequence 86, Application US/10044592
Publication No. US20020143152A1
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
TITLE OF INVENTION: Polypeptides, their Production and Use
FILE REFERENCE: 2463US2P
CURRENT APPLICATION NUMBER: US/10/044,592
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 09/403639
PRIOR FILING DATE: 1999-25-10
PRIOR APPLICATION NUMBER: PCT/JP98/01923
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: JP 9-109974
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 96
SOFTWARE:
SEQ ID NO 86
LENGTH: 98
TYPE: PRT
ORGANISM: Bovine
US-10-044-592-86

Query Match
Best Local Similarity 100.0%; Score 172; DB 14; Length 98;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSHMEIRTPDINPAWYAGRGIRPVGRF 31

;; PRIOR FILING DATE: 1999-25-10
;; PRIOR APPLICATION NUMBER: PCT/JP98/01923
;; PRIOR FILING DATE: 1998-04-27
;; PRIOR APPLICATION NUMBER: JP 9-109974
;; PRIOR FILING DATE: 1997-04-28
;; NUMBER OF SEQ ID NOS: 96
;; SOFTWARE:
;; SEQ ID NO 5
;; LENGTH: 31
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; NAME/KEY: PEPTIDE
;; LOCATION: (1)..(31)
;; OTHER INFORMATION: antigen
US-10-044-592-5

Query Match 94.8%; Score 163; DS 14; Length 31;
Best Local Similarity 93.5%; Pred. No. 1.6e-16;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 SRAQSHMEIRTPDINPAWYAGRC:RPVGRF 31
Db 1 SRAQSHMEIRTPDINPAWYAGRC:RPVGRF 31

Search completed: November 12, 2003, 11:14:55
Job time : 28 secs

GenCore version 5.1.6
Copyright: (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 12, 2003, 11:05:48 : Search time 18 Seconds
(without alignments)
82.426 Million cell updates/sec

Title: US-09-446-543A-5

Perfect score: 172

Sequence: 1 SRAHSHMEIRTPDINPAWYAGRGIPVGRF 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 252157 seqs, 47850546 residues

Total number of hits satisfying chosen parameters: 252157

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_New.*

1: /cgn2_6/prodata/1/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/prodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/prodata/1/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/prodata/1/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/prodata/1/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/prodata/1/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/prodata/1/paa/US10_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	33.1	492	7	US-60-478-196-3124
2	51.5	25.9	664	6	US-10-389-647-469
3	48.5	28.2	380	1	PCT-US03-30292-394
4	48.5	28.2	380	1	PCT-US03-30292-1500
5	48.5	28.2	380	6	US-10-666-642-394
6	48.5	28.2	380	6	US-10-666-642-1500
7	48.5	28.2	1091	6	US-10-679-563-8843
8	48	27.9	117	3	US-09-978-932A-611
9	48	27.9	190	6	US-10-679-063-5285
10	48	27.9	234	6	US-10-425-114A-62112
11	48	27.9	293	6	US-10-679-063-10848
12	48	27.9	314	6	US-10-679-063-10224
13	48	27.9	525	6	US-10-425-114A-51299
14	48	27.9	535	6	US-10-425-114A-60539
15	48	27.9	541	6	US-10-425-114A-50166
16	48	27.9	591	6	US-10-425-114A-50233
17	48	27.9	637	6	US-10-679-063-11393
18	48	27.9	746	6	US-10-425-114A-64563
19	48	27.9	746	6	US-10-425-114A-60157
20	47	27.3	345	5	US-09-976-858-171
21	47	27.3	455	6	US-10-679-063-10212
22	47	27.3	455	6	US-10-679-063-10845
23	46.5	27.0	337	6	US-10-296-115-1208
24	46.5	27.0	770	6	US-10-679-063-9397
25	46.5	27.0	770	6	US-10-679-063-12917
26	46.5	27.0	770	6	US-10-679-063-13708

27	46.5	27.0	770	6	US-10-679-063-23937
28	46.5	27.0	843	5	US-09-581-286A-432
29	46.5	27.0	849	5	US-09-581-286A-432
30	46	26.7	316	6	US-10-425-114A-57021
31	46	26.7	623	6	US-10-425-114A-56709
32	46	26.7	774	6	US-10-425-114A-56709
33	46	26.7	943	6	PCT-US03-10308A-26
34	46	26.7	943	6	US-10-406-686A-26
35	46	26.7	1420	7	US-60-478-196-3124
36	45	26.2	51	1	PCT-US03-31535-3
37	45	26.2	178	6	US-10-478-928-286
38	45	26.2	367	6	US-10-679-063-13181
39	45	26.2	367	6	US-10-679-063-15278
40	45	26.2	404	5	US-09-897-516A-5041
41	45	26.2	940	5	US-09-581-286A-463
42	45	26.2	943	5	US-09-897-516A-5223
43	45	26.2	962	5	US-09-581-286A-336
44	44.5	25.9	131	6	US-10-425-114A-48795
45	44.5	25.5	152	7	US-60-490-890-1908

ALIGNMENTS

RESULT 1
US-60-478-196-3124
: Sequence 3124, Application US/60478196
: GENERAL INFORMATION:
: APPLICANT: Jiang, Bo
: APPLICANT: Lemieux, Sebastien
: APPLICANT: Hu, Wenqi
: TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF ASPERGILLUS FUMIGATUS AND
: TITLE OF INVENTION: USE
: FILE REFERENCE: 10182-026-888
: CURRENT APPLICATION NUMBER: US/60478,196
: CURRENT FILING DATE: 2003-06-13
: NUMBER OF SEQ ID NOS: 4000
: SOFTWARE: PatensIn version 3.1
: SEQ ID NO 3124
: LENGTH: 492
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-60-478-196-3124

Query Match 33.1%, Score 57, DB 7, Length 492.
Best Local Similarity 43.5%, Pred. No. 9.2:
Matches 10: Conservative 4; Mismatches 9; Indels 5; Gaps 0.

QY 3 AHQSHMEIRTPDINPAWYAGRG 25
DB 248 SHHGVQALGPNNANLACGSI 270

RESULT 2
US-10-389-647-469
: Sequence 469, Application US/10389647
: GENERAL INFORMATION:
: APPLICANT: GREENBERG, E. Peter
: APPLICANT: SCHUSTER, Martin
: APPLICANT: LOSTROH, Candé
: TITLE OF INVENTION: OROUM SENSING SIGNALING IN BACTERIA
: FILE REFERENCE: U12-038CP
: CURRENT APPLICATION NUMBER: US/10389,647
: CURRENT FILING DATE: 2003-03-14
: PRIOR APPLICATION NUMBER: 09/653730
: PRIOR FILING DATE: 2000-09-01
: PRIOR APPLICATION NUMBER: 60/153022
: PRIOR FILING DATE: 1999-09-03
: NUMBER OF SEQ ID NOS: 710
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 469
: LENGTH: 664

APPLICANT: OGAU, RICHIE
: TITLE OF INVENTION: BREAST, GASTRIC, AND PROSTATE CANCER ASSOCIATED ANTIGENS AND
: TITLE OF INVENTION: USES THEREFOR

1
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-2153313:B

; CURRENT APPLICATION NUMBER: US/10/425,114A

; CURRENT FILING DATE: 2003-04-23

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 50166

; LENGTH: 541

; TYPE: PRT

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: 700890310_FLI.pep

US-10-425-114A-50166

Query Match.

27.9%; Score 48; DB 6; Length 541;

Best Local Similarity 33.3%; Pred. No. 1.2e+02;

Matches 9; Conservative 5; Mismatches 7; Indels 5; Gaps 1;

QY 8 MEIRTPDINPMYAG-----RGIRPV 28

Db 426 LGARTKLLNPKWYEGMLSTGYEGVREI 452

Search completed: November 12, 2003. 11:14:14

Job time : 18 secs

GenCore version 3.1.6
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OM protein: - protein search, using sw mode:

Run on: November 12, 2003, 11:06:47 ; Search time 21 Seconds
(without alignments)
141,963 Million cell updates/sec

Title: US-09-446-543A-5

Perfect score: 172

Sequence: 1 SRAHQSMETRTDINPAWYAGRIRPVGRF 31

Scoring table: BLOSUM62

Gapop 12.0 , Gapext 0.5

Searched: 283308 seqs, 96166682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 2

Maximum DB seq length: 2200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 76:**

1: p1r1:**

2: p1r2:**

3: p1r3:**

4: p1r4:**

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163	94.8	83	2 JC7607	prolactin-releasin
2	56.5	52.8	303	2 AH2016	hypothetical prote
3	55	32.0	1236	2 T52904	yg protoporphyrin
4	54.5	31.7	503	2 A82193	hypothetical prote
5	53.5	31.1	175	2 S67150	adenine deaminase
6	53	30.8	376	2 C75580	hypothetical prote
7	52	30.2	73	2 A78137	hypothetical prote
8	52	30.2	308	2 AH2896	transcription regu
9	52	30.2	308	2 B97672	rook family protein
10	52	30.2	419	2 AH3166	hypothetical prote
11	52	30.2	1292	2 T31462	probable magnesium
12	51.5	29.9	664	2 F83376	conserved hypothet
13	51	29.7	294	2 T21075	hypothetical prote
14	51	29.7	430	1 B69309	conserved hypothet
15	51	29.7	796	2 S11210	probable untr prote
16	51	29.7	962	2 H69157	exonuclease ABC c
17	50.1	29.4	790	2 T47959	hypothetical prote
18	50	29.1	527	2 T33175	hypothetical prote
19	50	29.1	974	2 AH3361	hypothetical prote
20	49.5	28.8	393	2 AB2664	exonuclease ABC c
21	49.5	28.8	401	2 A97446	conserved hypothet
22	49	28.5	128	2 S76955	hypothetical prote
23	49	28.5	226	2 A87664	hypothetical prote
24	48.5	28.2	254	2 S76814	hypothetical prote
25	48.5	28.2	548	2 T47548	hypothetical prote
26	48.5	28.2	1882	2 S73484	hypothetical prote
27	48	27.9	72	2 E910C2	probable regulator
28	48	27.9	220	2 C83292	probable glutathio
29	48	27.9	314	2 B70569	hypothetical prote

30	48	27.9	348	2 T21648	hypothetical prote
31	48	27.9	365	2 T39098	hypothetical prote
32	48	27.9	397	2 JC7675	acetoacetyl-CoA re
33	48	27.9	424	2 B38176	samb protein: Sal
34	48	27.9	637	2 D87559	sensory box histid
35	48	27.9	772	2 T07958	protoporphyrin IX
36	48	27.9	960	2 AH2115	exonuclease ABC c
37	48	27.9	973	2 AH2762	ABC exonuclease s
38	48	27.9	982	2 G97543	exonuclease ABC c
39	48	27.9	1328	2 A22351	protoporphyrin IX
40	48	27.9	1331	2 S75000	protoporphyrin IX
41	48	27.9	1379	2 S37310	protoporphyrin IX
42	48	27.9	1380	2 S64721	protoporphyrin IX
43	48	27.9	1381	2 S71288	protoporphyrin IX
44	48	27.9	1382	2 T01789	protoporphyrin IX
45	48	27.9	1383	2 T07126	magnesium chelatase

ALIGNMENTS

RESULT 1

JC7607
prolactin-releasing peptide - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7607
R:Yamada, M.; Ozawa, A.; Ishii, S.; Shibusawa, N.; Hashida, T.; Ishizuka, T.; Hosoya, T.; Biochem. Biophys. Res. Commun. 281, 53-56, 2001
A:Title: Isolation and characterization of the rat prolactin-releasing peptide gene:
A:Reference number: JC7607; MUID:21092785; PMID:1178959
A:Contents: Spleen
A:Accession: JC7607
A:Molecule type: DNA
A:Residues: 1-83 <YAM>
A:Cross-references: DBJ:AB040612; DDBJ:AB040613
C:Comment: This peptide induces arachidonic acid metabolite release from rat anterior release, and stimulation of ACTH secretion from the pituitary.
C:Genetics:
A:Gene: PrRP
A:Introns: 13/1

Query Match 94.8%; Score 163; DB 2; Length 83;
Best Local Similarity 93.5%; Pred. No. 6.9e-17;
Matches 29; Conservative 0; Mismatches 2; Indels 3; Gaps 0;

QY 1 SRAHQSMETRTDINPAWYAGRIRPVGRF 31
DB 22 SRAHQSMETRTDINPAWYAGRIRPVGRF 52

RESULT 2

AH2016
hypothetical protein all1686 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AH2016
P:Karako, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH2016
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-303 <KUR>
A:Cross-references: GB:BA000009; PIDB:BA078052.1; PDB:1J35506; GSPDB:GNCT179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1686

Query Match 92.8%; Score 56.5; DB 2; Length 303;

A:Map position: linear chromosome

```
Query Match      30.2%  Score 52; DB 2; Length 23;
Best Local Similarity 47.6%  Pred. No. 1.5;
Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 AHQHSNEITPDINPAWYAGR 23
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 23 AUTHRDVRSACISVRLAQR 43
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 8
AH2896
transcription regulator, ROK family Atu2609 (imported) - Agrobacterium tumefaciens (strain C58)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AH2896
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.;
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClall
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AH2896
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-308 <KUR>
A:Cross-references: GB:AE008688; PIDN:AAL43590.1; PID:gl7741107; GSPDB:GN00386
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu2609
A:Map position: circular chromosome
C:Superfamily: conserved hypothetical protein H10182; glucose kinase homology

Query Match      30.2%  Score 52; DB 2; Length 308;
Best Local Similarity 50.0%  Pred. No. 6.9;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 3 AHQHSNEITPDINPAWYAG 22
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 196 AHLHROEMTSIDIAAQWQ 215
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 9
B97672
rok family protein VC1532 (imported) - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: B97672
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourullo, B.; Goldman,
A.; Liu, F.; Mollan, C.; Allinger, M.; Doughty, D.; Doughty, C.; Lappas, C.; Markelz, B.
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: B97672
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-308 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK88331.1; PID:gl5157809; GSPDB:GN00169
C:Genetics:
A:Gene: AGR C 4728
A:Map position: conserved hypothetical protein H10182; glucose kinase homology
C:Superfamily: conserved hypothetical protein H10182; glucose kinase homology

Query Match      30.2%  Score 52; DB 2; Length 308;
Best Local Similarity 50.0%  Pred. No. 6.9;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 3 AHQHSNEITPDINPAWYAG 22
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 196 AHLHROEMTSIDIAAQWQ 215
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
```

```
RESULT 10
AH3166
hypothetical protein upgB (imported) - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AH3166
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.;
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClall
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AH3166
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-419 <KUR>
A:Cross-references: GB:AE008687; PIDN:AAL45750.1; PID:gl7743483; GSPDB:GN00188
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: upgB
A:Genome: plasmid

Query Match      30.2%  Score 52; DB 2; Length 419;
Best Local Similarity 36.8%  Pred. No. 9.6;
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 12 TPDINPAWYAGRGIRPVGR 30
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 323 SPEANATWFACTGYLPINK 341
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 11
T31462
probable magnesium chelatase (EC 4.99.1.1) chain H BchH - Helicobacter mobilis
C:Species: Helicobacter mobilis
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
C:Accession: T31462
R:Xiong, J.; Inoue, K.; Bauer, C.E.
Proc. Natl. Acad. Sci. U.S.A. 95, 14891-14896, 1998
A:Title: Tracking molecular evolution of photosynthesis by characterization of a mag
A:Reference number: Z21036; MUID:99061957; PMID:9843379
A:Accession: T31462
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1292 <X10>
A:Cross-references: EMBL:AF090002; NID:G3820536; PID:G3820560; PIDN:AA084033.1
C:Genetics:
A:Gene: bchH
C:Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
C:Keywords: lyase

Query Match      30.2%  Score 52; DB 2; Length 1292;
Best Local Similarity 38.5%  Pred. No. 32;
Matches 10; Conservative 3; Mismatches 7; Indels 6; Gaps 1;

QY 9 EIRTPDINPAWYAG-----RCIRPV 28
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1176 ETRTNTLPKWYEGMLKHGVEGVREI 1201
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 12
F83376
conserved hypothetical protein PA2151 (imported) - Pseudomonas aeruginosa (strain PAC
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F83376
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lberg, K.;
Lofy, S.; Olson, M.V.
```

Nature 405, 959-964, 2000

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A:Reference number: A82950; MUID:2043737; PMID:10984043
 A:Accession: F83376
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-664 <STO>
 A:Cross-references: GB:AE004642; GB:AE004091; NID:G9948163; PIDN:AA05539.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA2151

Query Match 29.9%; Score 51.5; DB 2; Length 666;

Best Local Similarity 55.6%; Pred. No. 19; Mismatches 5; Indels 1; Gaps 1;

QY 10 IRTPDINPAMYAGRGIRP 27

DB 476 VNTPDINP-WFLQSGRP 492

RESULT 13

T21075
 Hypothetical protein F19H6.1 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
 C:Accession: T21075; T21124
 R:McMurray, A.
 submitted to the EMBL Data Library, August 1995
 A:Reference number: Z19368
 A:Accession: T21075
 A:Status: preliminary; translated from GB/EMBL/DD5J
 A:Molecule type: DNA
 A:Residues: 1-294 <W1L>
 A:Cross-references: EMBL:Z50973; PIDN:CAA90762.1; GSPDB:GN00028; CESP:F19H6.1
 A:Experimental source: clone F19E5
 R:McMurray, A.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z19378
 A:Accession: T21124
 A:Status: preliminary; translated from GB/EMBL/DD5J
 A:Molecule type: DNA
 A:Residues: 1-294 <W12>
 A:Cross-references: EMBL:Z68115; PIDN:CAA92169.1; GSPDB:GN00028; CESP:F19H6.1
 A:Experimental source: clone F19H6
 C:Genetics:
 A:Gene: CESP:F19H6.1
 A:Map position: X
 A:Introns: 55/3; 85/2; 113/3; 157/-; 192/3; 266/2
 C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 29.7%; Score 51; DB 2; Length 294;

Best Local Similarity 44.8%; Pred. No. 9.2; Mismatches 12; Indels 2; Gaps 1;

QY 3 AHQHSMEIRTPDINPA--WVAGRGIRPVG 29

DB 139 AHVSKAIVHRDINPANNVITGNGIVKLG 167

RESULT 14

B69009
 conserved hypothetical protein MTH1070 - *Methanobacterium thermoautotrophicum* (strain Delta H)
 C:Species: *Methanobacterium thermoautotrophicum*
 C:Date: 29-Jan-1999 #sequence_revision 29-Jan-1999 #text_change 23-Jul-1999
 C:Accession: B69009
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 /Giu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol 179, 7135-7155, 1997
 A:Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: function
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: B69009

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-430 <MTH>

A:Cross-references: GB:AE000877; GB:AE000666; NID:G2622157; PIDN:AA85559.1; FID:G262

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH1070

C:Superfamily: conserved hypothetical protein MTH1070

Query Match 29.7%; Score 51; DB 1; Length 430;

Best Local Similarity 69.2%; Pred. No. 14; Mismatches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 14 DINPAWYAGRGIR 26

DB 191 DINPWWAGRACR 203

RESULT 15

S11210
 Probable untr protein - rat
 C:Species: *Rattus norvegicus* (Norway rat)
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
 C:Accession: S11210
 R:Jeffers, M.; Paciucci, R.; Pellicer, A.
 Nucleic Acids Res. 18, 4891-4899, 1990
 A:Title: Characterization of unr; a gene closely linked to N-ras.
 A:Reference number: S11210; MUID:90370473; PMID:2204025
 A:Accession: S11210
 A:Molecule type: mRNA
 A:Residues: 1-798 <JEF>
 A:Cross-references: EMBL:X52311; NID:G57454; PIDN:CAA36549.1; P:ID:G57455
 C:Keywords: DNA binding

Query Match 29.7%; Score 51; DB 2; Length 798;

Best Local Similarity 43.5%; Pred. No. 27; Mismatches 10; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 6 HSMETTPDINPAMYAGRGIRPV 28

DB 583 HSWGITEANPTIYSGKVRPS 605

Search completed: November 12, 2003, 11:10:05

Job time: 22 secs

Result No.	Query	Score	Match	Length	DB	ID	Description
1	72	100.0	98	1	PRR_BOVIN	P81264	bos taurus
2	63	94.8	83	1	PRR_RAT	P81278	rattus norv
3	158	91.9	87	1	PRR_HUMAN	P81277	homo sapien
4	61	35.5	428	1	NER3_BOVIN	O98559	bos taurus
5	56	32.6	428	1	NER3_HUMAN	O98449	homo sapien
6	52	30.2	417	1	EX7L_CORGL	O8nm3	corynebacte
7	52	30.2	447	1	EX7L_CORGF	O8fcm1	corynebacte
8	51	29.7	798	1	UNR_RAT	P_83395	rattus norv
9	51	29.7	962	1	JVRA_METTH	O26543	me-hanobact
10	50	23.1	288	1	Y587_PASMU	O9cm56	pasteurella
11	50	23.1	973	1	JVRA_RHILO	O9cm36	rhizobium m
12	50	23.1	973	1	JVRA_RHIME	P58699	rhizobium m
13	48.5	28.2	239	1	EPGL_SYNY3	974618	synechocyst
14	46.5	28.2	1882	1	Y668_WCPN	975109	mycoplasma
15	48	27.9	424	1	SAMB_SALTY	P23832	salmonella p
16	49	27.9	960	1	JVRA_TREPA	O83527	treponema p
17	47.5	27.6	1083	1	T293_HUMAN	O00268	homo sapien
18	47	27.3	406	1	CH12_RABIT	P53976	oryctolagus
19	47	27.3	418	1	NER3_RAT	O99955	rattus norv
20	47	27.3	442	1	TRE2_METMA	O8q001	methanocarc
21	47	27.3	940	1	JVRA_YABCH	O9knw5	vibrio chol
22	47	27.3	969	1	JVRA_MYCLE	O9cc24	mycobacteri
23	47	27.3	972	1	JVRA_MYCTU	E94972	mycobacteri
24	47	27.3	1308	1	M4K6_MOUSE	O9jm52	mus musculus
25	46.5	27.0	345	1	ARGC_BACHD	O9K8v2	bacillus ba
26	46.5	27.0	770	1	AVP3_AZATH	P31414	arabidopsis
27	46	26.7	277	1	DAPF_CORGL	O58p73	corynebacte
28	46	26.7	342	1	Y762_METJA	O58172	methanococc
29	46	26.7	347	1	Y576_METJA	O57396	methanococc
30	46	26.7	402	1	EX7L_STRCO	O9fcm3	streptomyce
31	46	26.7	510	1	YCGB_ECOLI	P29013	escherichia
32	46	26.7	798	1	UNR_HUMAN	O75534	homo sapien
33	46	26.7	836	1	TSM1_RABIT	P22758	oryctolagus

```

RESULT 2
PRRP_EAT
ID PRRP_RAT STANDARD: PRT: 83 AA.
AC P81278: Q8K3YC;
DT 30-MAY-2000 (Rel. 39, Created);
DT 30-MAY-2000 (Rel. 39, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Prolactin-releasing peptide precursor (PRRP) (Prolactin-releasing
DE hormone) [Contains: Prolactin-releasing peptide PRP31; Prolactin-
DE releasing peptide PRP20].
GN PRH.
OS Rattus norvegicus (Rat);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [-];
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=98268781; PubMed=9607765;
RA Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S.,
RA Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
RA Kurokawa T., Nishimura O., Onda H., Fujino M.;
RA "A prolactin-releasing peptide in the brain.";
RL Nature 393:272-276(1998).
RN [2];
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=Sprague-Dawley; TISSUE=Hypothalamus;
RA Anderson S.F., Kokay I.C., Lang T., Gratian D.R., Curlewis J.D.;
RT "Quantitation of prolactin-releasing peptide (PRRP) mRNA expression in
RT specific brain regions during the rat oestrous cycle and in
RT lactation.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [3];
RP TISSUE SPECIFICITY;
RX MEDLINE=99426652; PubMed=10498338;
RA Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S.,
RA Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
RA Sumino Y., Fujino M.;
RA "Tissue distribution of prolactin-releasing peptide (PRRP) and its
RA receptor.";
RL Regul. Pept. 83:1-10(1999).
CC -!- FUNCTION: Stimulates prolactin (PRL) release and regulates the
CC expression of prolactin through its receptor GPR10. May stimulate
CC lactotrophs directly to secrete PRL.
CC -!- ALTERNATIVE PRODUCTS;
CC Name=1;
CC Name=2;
CC IsoId=P81278-1; Sequence=Displayed;
CC IsoId=P81278-2; Sequence=VSP_004370;
CC -!- TISSUE SPECIFICITY: Widely expressed, with highest levels in
CC media oblongata and hypothalamus.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to licenses@isb-sib.ch).
CC -----
CC EMBL: AB015418; BAA29026.1;
CC DR MIM: 602663;
CC DR GO: GO:0005180; F:peptide hormone; TAS.
CC PIR: JC7607; JC7607.
CC KW Hormone; Amidation; Signal; Cleavage on pair of basic residues;
CC Alternative splicing.
CC SIGNAL 1
CC FT PEPTIDE 22 52 BY SIMILARITY.
CC FT PEPTIDE 33 52 PROLACTIN-RELEASING PEPTIDE PRP31.
CC FT PROPEP 57 83 PROLACTIN-RELEASING PEPTIDE PRP20.
CC FT MOD_RES 52 52
CC FT VARSPIC 33 83
CC AMIDATION (G-53 PROVIDE AMIDE GROUP).
CC TPINPAWYTGRIYVGRGRATPRDVTGLGQLSCLPL
CC DGRNKFQSQG -> SECLTYGKQPLTSFHFQMPPP (in

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isoform 2);
/FTID=VSP_004370.
FT SEQUENCE 83 AA; 92:5 MW; DCC75A264EE54F29 CRC64;
SQ
Query Match 94.8%; Score 163; DB 1; Length 83;
Best Local Similarity 93.5%; Pred. No. 3,3e-17;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 SRAHQSHNEIRTPDINPAWYTGRIYVGRF 31
|||||
DB 22 SRAHQSHMETRTPDINPAWYTGRIYVGRF 52
|||||
RESULT 3
PRRP_HUMAN
ID PRRP_HUMAN STANDARD: PRT: 87 AA.
AC P81277;
DT 30-MAY-2000 (Rel. 39, Created);
DT 30-MAY-2000 (Rel. 39, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Prolactin-releasing peptide precursor (PRRP) (Prolactin-releasing
DE hormone) [Contains: Prolactin-releasing peptide PRP31; Prolactin-
DE releasing peptide PRP20].
GN PRH.
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98268781; PubMed=9607765;
RA Hinuma S., Habata Y., Fujii R., Kawamata Y., Hosoya M., Fukusumi S.,
RA Kitada C., Masuo Y., Asano T., Matsumoto H., Sekiguchi M.,
RA Kurokawa T., Nishimura O., Onda H., Fujino M.;
RA "A prolactin-releasing peptide in the brain.";
RL Nature 393:272-276(1998).
RN [2];
RP TISSUE SPECIFICITY;
RX MEDLINE=99426652; PubMed=10498338;
RA Fujii R., Fukusumi S., Hosoya M., Kawamata Y., Habata Y., Hinuma S.,
RA Sekiguchi M., Kitada C., Kurokawa T., Nishimura O., Onda H.,
RA Sumino Y., Fujino M.;
RA "Tissue distribution of prolactin-releasing peptide (PRRP) and its
RA receptor.";
RL Regul. Pept. 83:1-10(1999).
CC -!- FUNCTION: Stimulates prolactin (PRL) release and regulates the
CC expression of prolactin through its receptor GPR10. May stimulate
CC lactotrophs directly to secrete PRL.
CC -!- TISSUE SPECIFICITY: MEDULLA OBLONGATA AND HYPOTHALAMUS.
CC -----
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CC or send an email to licenses@isb-sib.ch).
CC -----
CC EMBL: AB015419; BAA29027.1;
CC DR MIM: 602663;
CC DR GO: GO:0005180; F:peptide hormone; TAS.
CC KW Hormone; Amidation; Signal.
CC SIGNAL 1 22 BY SIMILARITY.
CC FT PEPTIDE 23 53 PROLACTIN-RELEASING PEPTIDE PRP31.
CC FT PEPTIDE 34 53 PROLACTIN-RELEASING PEPTIDE PRP20.
CC FT PROPEP 58 87
CC FT MOD_RES 53 53
CC FT SEQUENCE 87 AA; 9639 MW; 22942F3F50CF981B CRC64;
QY Match. 91.9%; Score 158; DB 1; Length 87;
Best Local Similarity 90.3%; Pred. No. 1.9e-16;
Matches 28; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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FT ACT SITE 45 45 Potential.
FT ACT SITE 50 50 Potential.
FT ACT SITE 87 87 Potential.
FT ACT SITE 225 225 Potential.
FT ACT SITE 245 245 Potential.
FT ACT SITE 340 340 By similarity.
FT ACT SITE 370 370 Potential.
FT ACT SITE 387 387 Potential.
SQ SEQUENCE 428 AA: 48252 MW: 35DIDD9359A78C98 CRC64;
Query Match 32.6%; Score 56; DB 1; Length 428;
Best Local Similarity 37.0%; Pred. No. 1.1;
Matches 10; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 2 RAHQSHWEIRTPDINPAWYAGRGIRPV 28
DB 195 KTRPHSLMIYSDLGVTWHGRILRPM 221

RESULT 6
EX7L_COREF STANDARD; PRT; 417 AA.
ID EX7L_COREF STANDARD; PRT; 417 AA.
AC G6NRN3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
DE (Exonuclease VII large subunit)
DE XSEA OR CG1025.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
*!- FUNCTION: Bidirectionally degrades single-stranded DNA into large
acid-insoluble oligonucleotides, which are then degraded further
into small acid-soluble oligonucleotides (By similarity).
*!- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'-
or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
*!- SUBUNIT: Heterooligomer composed of large and small subunits (By
similarity).
*!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
*!- SIMILARITY: BELONGS TO THE XSEA FAMILY.
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CC
CC EMBL; AF005277; BAB984.8.1;
CC HAYAP; MF 00378; 1;
CC InterPro: IPR003753; Exonuc VII_L.
CC Pfam; PF02601; Exonuc VII_L; 1.
CC TIGRFAMs; TIGR00237; xsea; 1.
CC HydroLase; Nuclease; Exonuclease; Complete proteome.
CC SEQUENCE 417 AA: 45582 MW: 332CD9286C173C34 CRC64;
CC
CC
CC Query Match 30.2%; Score 52; DB 1; Length 417;
CC Best Local Similarity 57.1%; Pred. No. 4.1;
CC Matches 12; Conservative 1; Mismatches 0; Indels 8; Gaps 1;

QY 17 PANYAGRG-----IRPVG 29
DB 94 PAFYAGRGTSFLWVTDIRPVG 114

Query Match 30.2%; Score 52; DB 1; Length 417;
Best Local Similarity 57.1%; Pred. No. 4.1;
Matches 12; Conservative 1; Mismatches 0; Indels 8; Gaps 1;

QY 17 PANYAGRG-----IRPVG 29
DB 94 PAFYAGRGTSFLWVTDIRPVG 114

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RESULT 7
EX7L_COREF STANDARD; PRT; 447 AA.
ID EX7L_COREF STANDARD; PRT; 447 AA.
AC Q8FQP1;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
DE (Exonuclease VII large subunit)
DE XSEA OR CE1078.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawarabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314."
Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
*!- FUNCTION: Bidirectionally degrades single-stranded DNA into large
acid-insoluble oligonucleotides, which are then degraded further
into small acid-soluble oligonucleotides (By similarity).
*!- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'-
or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
*!- SUBUNIT: Heterooligomer composed of large and small subunits (By
similarity).
*!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
*!- SIMILARITY: BELONGS TO THE XSEA FAMILY.
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CC
CC EMBL; AP005217; BAC17888.1;
CC HAYAP; MF 00378; 1;
CC InterPro: IPR003753; Exonuc VII_L.
CC Pfam; PF02601; Exonuc VII_L; 1.
CC TIGRFAMs; TIGR00237; xsea; 1.
CC HydroLase; Nuclease; Exonuclease; Complete proteome.
CC SEQUENCE 447 AA: 49031 MW: FDBDF6A768E742C1 CRC64;
CC
CC
CC Query Match 30.2%; Score 52; DB 1; Length 447;
CC Best Local Similarity 57.1%; Pred. No. 4.4;
CC Matches 12; Conservative 1; Mismatches 0; Indels 8; Gaps 1;

QY 17 PANYAGRG-----IRPVG 29
DB 124 PAFYAGRGTSFLWVTDIRPVG 144

RESULT 8
UNR_RAT STANDARD; PRT; 798 AA.
ID UNR_RAT STANDARD; PRT; 798 AA.
AC P18395;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE UNR protein.
DE UNR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1;
RP SEQUENCE FROM N.A.

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DR InterPro: IPR004602; UvrA.
DR Pfam: PF00005; ABC_tran; 2.
DR ProDom: PD00006; ABC_transporter; 1.
DR TIGRfam: TIGR00630; UvrA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER_1; 2.
DR PROSITE: PS00993; ABC_TRANSPORTER_2; 1.
DR SOS response; Excision nuclease; DNA repair; DNA recombination;
KW DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
KW Zinc-finger; Complete proteome.
FT NP_BIND 34 41 ATP (POTENTIAL).
FT NP_BIND 662 669 ATP (POTENTIAL).
FT ZN_FING 762 787 C4-TYPE5.
FT CONFLICT 19 19 G -> A (IN REF. 2).
FT CONFLICT 67 67 F -> S (IN REF. 2).
SQ SEQUENCE 973 AA; 107191 MW; 3E1AB814527A47FE CRC64;

Query Match 29.1%; Score 50; DB 1; Length 972;
Best Local Similarity 39.5%; Pred. No. 19;
Matches 15; Conservative 2; Mismatches 3; Indels 18; Gaps 3;

QY 11 RTPDINPA-----WYAG-----RGIRPVGRF 31
||| ||| ||| ||| ||| ||| ||| ||| |||
DB 716 RPRSNFAYTGAFPIRDWFAQLPEAKARGYCP-GRF 752

RESULT 13
6PGL_SYNY3
ID 6PGL_SYNY3 STANDARD; PRT; 239 AA.
AC 274618;
DT 01-NOV-1997 (Rel. 35, Created);
RT 31-NOV-1997 (Rel. 35, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
GN PGL OR DEVB OR SL1479.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_taxonomy:1148;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Yatsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
RN 12;
RP SEQUENCE OF 1-19.
RX MEDLINE=97443974; PubMed=9298645;
RA Sazuka T., Ohara O.;
RT "Towards a proteome project of cyanobacterium Synechocystis sp.
RT strain PCC6803: linking 130 protein spots with their respective
RT genes.";
RL Electrophoresis 18:1252-1258(1997).
CC -1- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
CC 6-PHOSPHOGLUCONATE.
CC -1- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H2O = 6-
CC phospho-D-gluconate.
CC -1- PATHWAY: Pentose phosphate pathway; second step.
CC -1- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE
CC ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
-----
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DR EMBL: S90916; BAA18726.1; ALT_INIT.
DR InterPro: IPR006148; Gluc_gal_isom.
DR InterPro: IPR005900; Phosphogluconac.
DR Pfam: PF01182; Glucosamine iso; 1.
DR TIGRfam: TIGR01198; pgl_1.
KW Hydrolase; Complete proteome.
FT INIT_MET 0
SQ SEQUENCE 239 AA; 26351 MW; 9C64A0A342325917 CRC64;

Query Match 29.2%; Score 48.5; DB 1; Length 239;
Best Local Similarity 42.3%; Pred. No. 7.5;
Matches 11; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

QY 5 QHSM-EIRTPDINPAWYAGRIRPVG 29
||| ||| ||| ||| ||| ||| ||| |||
DB 198 QHAGLEIPAEADPOQYPARFIQDQ 223

RESULT 14
Y468_MYCPN
ID Y468_MYCPN STANDARD; PRT; 1892 AA.
AC P75139; Q50317;
DT 01-NOV-1997 (Rel. 35, Created);
RT 01-NOV-1997 (Rel. 35, Last sequence update);
DT 28-FEB-2003 (Rel. 41, Last annotation update);
DE Protein MG468 homolog (K05_orf1892);
GN MPN684 OR MP158.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
CX NCBI_taxonomy:2104;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948631;
RA Himmelfreich R., Hilbert H., Piagens H., Pirkl E., Ja B.-C.,
RA Hermann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
RN 12;
RP SEQUENCE OF 1-1848 FROM N.A.
RX STRAIN=ATCC 29342 / M129;
RX MEDLINE=96177562; PubMed=8604323;
RA Hilbert H., Himmelfreich R., Piagens H., Hermann R.;
RT "Sequence analysis of 56 kb from the genome of the bacterium
RT Mycoplasma pneumoniae comprising the draA region, the atp operon and a
RT cluster of ribosomal protein genes.";
RL Nucleic Acids Res. 24:628-639(1996).
RN 13;
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX STRAIN=ATCC 29342 / M129;
RX MEDLINE=21088919; PubMed=11271496;
RA Regula J.T., Ueberle B., Boguth G., Goerg A., Schnoelzer M.,
RA Hermann R., Frank R.;
RT "Towards a two-dimensional proteome map of Mycoplasma pneumoniae.";
RL Electrophoresis 21:3765-3780(2000).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential);
CC -1- SIMILARITY: SOME TO MG064.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: AF000017; AAB95806.1;
CC EMBL: U34816; AAC43650.1;
CC PIR: S73484; S73484.
DR InterPro: IPR003838; DUF214.
DR Pfam: PF02687; FtsX; 1.
KW Transmembrane; Complete proteome;

```

Search completed: November 12, 2003, 11:08:43
Job time : 12 secs

```
FT TRANSMEM 16 36 POTENTIAL.  
FT TRANSMEM 987 1007 POTENTIAL.  
FT TRANSMEM 1037 1057 POTENTIAL.  
FT TRANSMEM 1080 1100 POTENTIAL.  
FT TRANSMEM 1154 1174 POTENTIAL.  
FT TRANSMEM 1759 1779 POTENTIAL.  
FT TRANSMEM 1807 1827 POTENTIAL.  
FT TRANSMEM 1828 1848 POTENTIAL.  
FT TRANSMEM 1852 1871 POTENTIAL.  
SQ SEQUENCE 1882 AA; 209442 MW; 03CFA4D99A7120ED CRC64;
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Query Match 28.2%; Score 48.5; DB 1; Length 1882;
Best Local Similarity 32.3%; Pred. No. 64;
Matches 10; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

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Oy 1 SRAHQSHVEIRTPDINPAWYAGRGIRPVGRF 31  
Db 1188 MNFNVRNLNLTPTQSGWYA--IQVSRF 1215
```

RESULT 15

```
SAMP_SALTY  
ID SAMP_SALTY STANDARD; PRT; 424 AA.  
AC P23832;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE SAMP protein.  
GN SAMP.  
OS Salmonella typhimurium.  
OC Plasmid 60-mDa cryptic.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Salmonella.  
OX NCBI_TaxID=602;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=572;  
RA MEDLINE=91123176; PubMed=1991707;  
RA Nohmi T., Hakura A., Nakai Y., Watanabe M., Murayama S.Y.,  
RA Sofuni T.  
RT "Salmonella typhimurium has two homologous but different umuDC  
RT operons: cloning of a new umuDC-like operon (samAB) present in a  
RT 60-megadalton cryptic plasmid of S. typhimurium";  
RL J. Bacteriol. 173:1051-1063 (1991).  
CC -1- FUNCTION: INVOLVED IN UV PROTECTION AND MUTATION.  
CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-Y FAMILY.  
CC -1- SIMILARITY: Contains 1 umuC domain.
```

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DR EMBL; D90202; BAAL4226.1; -  
DR PIR; B38176; B38176.  
DR HANAP; MF 01113; atypical; i.  
DR InterPro; IPR001126; UMuC_like.  
DR Pfam; PF00817; IMS; i.  
DR PROSITE; PS0173; UMuC; i.  
KW Plasmid; SOS mutagenesis; DNA repair.  
FT DOMAIN 2 189 UMuC  
SQ SEQUENCE 424 AA; 47727 MW; FF8C47476CC58A2B CRC64;
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Query Match 27.9%; Score 48; DB 1; Length 424;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

```
Oy 10 IRTFDINPAWYAGRGIRP 27  
Db 381 INHFGKGIWPAAGRIAP 398
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 12, 2003, 11:06:12 ; Search time 35 Seconds
(without alignments)
228.561 Million cell updates/sec

Title: US-09-446-543a-5
Perfect score: 172
Sequence: 1 SRAHQSMWEIRTPDINPAWYAGRGIRPVGRF 31

Scoring table: BLOSTP62
Gapop 10.0 , Gapext 0.5

Searched: 810525 seqs, 258052634 residues

Total number of hits satisfying chosen parameters: 810525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SP-REMBL 21:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mnc:
8: sp_organelle:
9: sp_phase:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacterioph:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	100.0	98	Q8WN12	Q8WN12 ovis aries
2	104	60.5	117	Q9W624	Q9W624 carassius a
3	62	36.0	692	Q5L306	Q5L306 rhodospirill
4	57	33.1	54	Q9JUF9	Q9JUF9 homo sapien
5	57	33.1	355	Q95YJ8	Q95YJ8 ciona savig
6	57	33.1	465	Q60687	Q60687 homo sapien
7	57	33.1	465	Q8W85	Q8W85 homo sapien
8	56.5	32.8	303	Q8YWC7	Q8YWC7 anabaena sp
9	55	32.0	1236	Q9CPM4	Q9CPM4 rhodocycius
10	54.5	31.7	501	Q9KRY1	Q9KRY1 vibrio chol
11	53.5	31.1	176	Q08689	Q08689 saccharomyc
12	53	30.8	376	Q9RY22	Q9RY22 deinococcus
13	53	30.8	467	Q8R054	Q8R054 mus musculu
14	53	30.8	468	Q8K1F8	Q8K1F8 mus musculu
15	52	30.2	73	Q8U515	Q8U515 agrobacteri
16	52	30.2	308	Q8UC89	Q8UC89 agrobacteri

17	52	30.2	419	16	Q8UKR2
18	52	30.2	440	11	Q8CBT2
19	52	30.2	447	16	Q8FQP1
20	52	30.2	848	11	Q8C720
21	52	30.2	1253	2	Q8RTV7
22	52	30.2	1292	2	Q9ZGE5
23	52	30.2	3567	11	Q9ES77
24	51.5	29.9	327	10	Q94KU5
25	51.5	29.9	327	10	Q94PZ9
26	51.5	29.9	664	16	Q91LM4
27	51	29.7	184	16	Q8PER0
28	51	29.7	294	5	Q1953D
29	51	29.7	315	2	Q87474
30	51	29.7	333	4	Q96SD4
31	51	29.7	367	4	Q8N6Q2
32	51	29.7	367	4	Q81XT2
33	51	29.7	370	11	Q8CGW9
34	51	29.7	430	17	Q27142
35	51	29.7	514	5	Q9VRV3
36	51	29.7	689	11	Q8R3R1
37	51	29.7	767	11	Q8JZN2
38	51	29.7	798	11	Q91K50
39	51	29.7	1563	5	Q8T4U2
40	51	29.7	1845	17	Q8ITS7
41	50.5	29.4	232	10	Q8S7E3
42	50.5	29.4	374	16	Q8Z5E1
43	50.5	29.4	420	2	Q93J27
44	50.5	29.4	790	10	Q9M371
45	50	29.1	217	16	Q8PQ42

ALIGNMENTS

RESULT 1

Q8WN12	PRELIMINARY;	PRT;	58 AA.
ID	Q8WN12		
AC	Q8WN12;		
DT	01-MAR-2002 (TRENBLrel. 20, Created)		
DT	01-MAR-2002 (TRENBLrel. 20, Last sequence update)		
DT	01-MAR-2002 (TRENBLrel. 20, Last annotation update)		
DE	Preprolactin-releasing peptide		
OS	Ovis aries (Sheep)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Caprinae; Ovis		
OX	NCBI_TaxID=9940;		
RK	{1}		
RP	SEQUENCE FROM N.A.		
RA	Curleris J.D., Kusters D.H.L., Barclay J.L., Anderson S.T.,		
RT	"Prolactin-releasing peptide (PRP) in the ewe: cDNA cloning, mRNA		
RT	distribution and effects on prolactin secretion in vitro and in		
RT	vivo"		
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF450453; AAL47178.1;		
SQ	SEQUENCE 98 AA; 10513 MW; 2A53331ED52CAAB5 CRC64;		

Query March 100.0% Score 172; DB 6; Length 98;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SRAHQSMWEIRTPDINPAWYAGRGIRPVGRF 31
|||||
DB 23 SRAHQSMWEIRTPDINPAWYAGRGIRPVGRF 53
|||||

RESULT 2
Q9W624 PRELIMINARY; PRT; 117 AA.
ID Q9W624
AC Q9W624

DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

```

DE C-Rf amide.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Satake H., Minakata H., Fujimoto M.;
RT 'Carassius Ramide (C-Rf amide)';
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: ABO20024; SAA76662.1;
SQ SEQUENCE 117 AA; 12879 MW; D5DC4CB22038C2B0 CRC64;

Query Match 60.5%; Score 104; DB 13; Length 117;
Best Local Similarity 57.7%; Pred. No. 4.8e-07;
Matches 15; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 6 HSMSEIRTPDINPAWVAGRGIRPVGRF 31
DQ 50 HNVNRSPEIDPFVVGKQVPIGRF 75
DQ 50 HNVNRSPEIDPFVVGKQVPIGRF 75

RESULT 3
QY 99L8J6 PRELIMINARY; PRT: 692 AA.
AC Q99L8J6
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE BchH (Fragment).
GN BCHH.
OS Rhodospirillum rubrum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Rhodospirillum.
OX NCBI_TaxID=1085;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R5;
RA Cheng Y.S., Brantner C.A., Tsapin A., Collins M.L.P.;
RT "Role of the H protein in assembly of the photochemical reaction
center and intracytoplasmic membrane in Rhodospirillum rubrum.";
RL J. Bacteriol. 182:1200-1207(2000).
DR EMBL: AF202319; AAF37352.1;
DR InterPro: IPR003672; COB_Nrg_chitase.
DR Pfam: PF02514; COB_Nrg_chet; 1.
FT NON TER 1
SQ SEQUENCE 692 AA; 75433 MW; 9643DAE93BF35680 CRC64;

Query Match 36.0%; Score 62; DB 2; Length 692;
Best Local Similarity 40.6%; Pred. No. 2.7;
Matches 13; Conservative 4; Mismatches 9; Indels 5; Gaps 1;

QY 3 AHOHSMSEIRTPDINPAWVAG-----RGIRPV 28
DQ 568 AEQVSLTRTRALNPKVVEGMAHGVGVQRI 599
DQ 568 AEQVSLTRTRALNPKVVEGMAHGVGVQRI 599

RESULT 4
QY 99UJF9 PRELIMINARY; PRT: 54 AA.
AC Q99UJF9
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE DJ479J7.3 (Sushi-repeat protein (SRPUL)) (Fragment).
GN DJ479J7.3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RA Lawlor S.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL035608; CAB55682.1;
FT NON TER 54
SQ SEQUENCE 54 AA; 6110 MW; E2F3C39F7B961A9F CRC64;

Query Match 33.1%; Score 57; DB 4; Length 54;
Best Local Similarity 56.2%; Pred. No. 0.98;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 12 TPDINPAWVAGRGIRP 27
DQ 18 TPAVTPWYAGSGYYP 33
DQ 18 TPAVTPWYAGSGYYP 33

RESULT 5
QY 99YJ8 PRELIMINARY; PRT: 355 AA.
AC Q99YJ8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Zic related protein 1a.
GN CS-ZICR1A.
OS Ciona savignyi.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cionidae; Ciona.
OX NCBI_TaxID=51511;
RN [1]
RP SEQUENCE FROM N.A.
RA Imai K.S., Satoh N., Satou Y.;
RT "Ciona savignyi genes.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB057747; BAB68356.1;
DR InterPro: IPR007087; Znf_C2H2.
DR Pfam: PF00096; zf-C2H2; 4.
DR SMART: SM00355; Znf_C2H2; 4.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 3.
DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 4.
DR Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 355 AA; 40876 MW; E58F5DEDD812E8AC CRC64;

Query Match 33.1%; Score 57; DB 5; Length 355;
Best Local Similarity 40.0%; Pred. No. 7;
Matches 12; Conservative 7; Mismatches 7; Indels 4; Gaps 1;

QY 2 RAHQHSMSEIRTPDIN----PAWVAGRGIRP 27
DQ 27 QAQOHSDSKPMQLNSVPSAAYVAGYGMIP 56
DQ 27 QAQOHSDSKPMQLNSVPSAAYVAGYGMIP 56

RESULT 6
QY 99C687 PRELIMINARY; PRT: 465 AA.
AC Q99C687
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Sushi-repeat protein (Sushi-repeat containing protein).
GN SRPJL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kurosawa H., Inukai T., Inaba T., Goi K., Chang K.-S., Sinjo T.,
RA Rakeshaw K.M., Naeve C.W., Look T.A.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

```

RA Huang C.-H., Chen H., Peng J., Chen Y.,
 RT "Cloning and characterization of the sushi-repeat containing protein
 RT (SRP) as a novel interaction partner of Rh type C glycoprotein
 RT (RhCGI).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBS databases.
 DR EMBL: AF960567; AAC5765.1; ..
 DR EMBL: AF93649; AAM73693.1; ..
 DR InterPro: IPR001128; Cytochrome_P450.
 DR InterPro: IPR003410; HyalIn.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF02494; HVR; 1.
 DR Pfam: PF00084; Sushi; 3.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 SQ SEQUENCE 465 AA; 52971 MW; 407525187FF3EFBS CRC64;

Query Match 33.1%; Score 57; DB 4; Length 465;
 Best Local Similarity 56.2%; Pred. No. 9.2;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 12 TPDIINPAWYAGRGIRP 27
 ||| |||||
 Db 18 TPVPTWYAGGYVP 33

RESULT 7

CSWWS ID Q8WWS PRE-IMINARY; PRT; 465 AA.
 AC Q8WWS;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Sushi-repeat protein.
 DE Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBS databases.
 DR EMBL: BC020733; AAM20733.1; ..
 DR InterPro: IPR001128; Cytochrome_P450.
 DR InterPro: IPR003410; HyalIn.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF02494; HVR; 1.
 DR Pfam: PF00084; Sushi; 3.
 DR SMART: SM00032; CCP; 3.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 SQ SEQUENCE 465 AA; 52957 MW; 357229487DA1B8BD CRC64;

Query Match 33.1%; Score 57; DB 4; Length 465;
 Best Local Similarity 56.2%; Pred. No. 9.2;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 12 TPDIINPAWYAGRGIRP 27
 ||| |||||
 Db 18 TPVPTWYAGGYVP 33

RESULT 8

Q8WYC ID Q8WYC PRE-IMINARY; PRT; 303 AA.
 AC Q8WYC;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein A11686.
 GN A11686.
 OS Anabaena sp. (strain PCC 71201).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=403690;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa N., Yamada Y.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 RT cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 DR EMBL: AP003586; BAB78052.1; ..
 DR InterPro: IPR004843; N-peptidase.
 DR Pfam: PF00149; Metallophos; 1.
 DR Hypothetical protein; Complete proteome.
 SQ SEQUENCE 303 AA; 34449 MW; 68570CB2127EE987 CRC64;

Query Match 32.8%; Score 56.5; DB 16; Length 303;
 Best Local Similarity 51.6%; Pred. No. 7;
 Matches 16; Conservative 2; Mismatches 8; Indels 5; Gaps 2;

QY 4 HQHSMETTPDINPAWY---AGRGIRPVGR 30
 ||| |||||
 Db 226 HERSYE-RTAIDGTTVLTCSAGAGRPVGR 255

RESULT 9

CSJPA ID Q3JPA PRE-IMINARY; PRT; 1236 AA.
 AC Q3JPA;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Mg protoporphyrin methyl transferase.
 DE BcNH.
 OS Rhodococcus gelatinosus (Rhodopseudomonas gelatinosa).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Comamonadaceae; Rubrivivax.
 OX NCBI_TaxID=28068;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL144;
 RA Nagashima K.V., Shimada K., Matsuura K.;
 RT "Phylogenetic analysis of photosynthetic genes of Rhodococcus
 RT gelatinosus: Possibility of horizontal gene transfer in purple
 RT bacteria.";
 RL Photosyn. Res. 36:185-191(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL144;
 RX MEDLINE=94132007; PubMed=8300574;
 RA Nagashima K.V., Matsuura K., Ohya S., Shimada K.;
 RT "Primary structure and transcription of genes encoding B870 and
 RT photosynthetic reaction center apoproteins from Rubrivivax
 RT gelatinosus.";
 RL J. Biol. Chem. 269:2477-2484(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL144;
 RA Igarashi N., Shimada K., Matsuura K., Nagashima K.V.;
 RT "Photosynthetic gene cluster in purple bacterium, Rubrivivax
 RT gelatinosus.";
 RL (In) Garab G. (eds.);
 RL Photosynthesis:
 RL mechanisms and effects (Proceedings of the 11th international congress
 RL on photosynthesis), pp.4:2889-2892, Kluwer Academic Publishers.
 RL Dordrecht (1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL144;
 RX MEDLINE=20031519; PubMed=10563807;
 RA Menin L., Yoshida M., Jaquinod M., Nagashima K.V., Matsuura K.,
 RA Parot P., Vermeglio A.;
 RT "Dark aerobic growth conditions induce the synthesis of a high

RT midpoint potential cytochrome c0 in the photosynthetic bacterium
 RT Rubrivivax gelatinosus".
 RL Biochemistry 38:15238-15244(1999).
 DR EMBL: A034704; BAA94037.1; -.
 DR InterPro: IPR003672; COB/Mg_chelase.
 DR Pfam: PF02514; cobN-Mg_chel: 1.
 KW "transferase".
 SQ SEQUENCE 1236 AA: 134729 MW: 8405100456385200 CRC64;

Query Match 32.0% Score 55; DB 2; Length 1236;
 Best Local Similarity 34.4% Pred. No. 49;
 Matches 11; Conservative 6; Mismatches 9; Indels 6; Gaps 1;

Qy 3 AHOHSMETPDINPANYAG-----RGIRPV 28
 Db 1112 SEQVAETRTMDAPKNGEGLKHYEGVRO 1143

RESULT 10

Q9KRY1 PRELIMINARY; PRT; 503 AA.
 AC Q9KRY1
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Sun/rubioleal protein family protein.
 GN VCI502
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN (1)
 RC SEQUENCE FROM N.A.
 RZ STRAIN=EL Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen G.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Uterback T., Fleischmann R.D., Kierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., McKelanos J.T., Venter J.C.,
 RA Fraser C.M.;
 RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae".
 RT Nature 406:477-483(2000).
 RL EMBL: A034228; AAF94657.1; -.
 DR TIGR: VC1502; -.
 DR InterPro: IPR000051; SAM_bind.
 DR Pfam: PF01189; NOL1_NOP2_Sun; 1.
 DR TIGRPFAMs: TIGR00446; nop2p; 1.
 DR PROSITE: PS0153; NOL1_NOP2_Sun; 1.
 KW Complete proteome.
 SQ SEQUENCE 503 AA: 55997 MW: 28BD94A23E6C9E48 CRC64;

Query Match 31.7% Score 54.5; DB 16; Length 503;
 Best Local Similarity 36.7% Pred. No. 23;
 Matches 12; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

Qy 1 SRAHQSMETPDINPANYAGRGIRPVGR 30
 Db 435 SSSASHSVSLCTQAR-EWFMGRDVRPEQG 463

RESULT 11

Q08689 PRELIMINARY; PRT; 176 AA.
 AC Q08689
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Chromosome XV reading frame ORF YOR253W.
 GN ARD2 OR YOR253W.

OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN (1)
 RC SEQUENCE FROM N.A.
 RZ MIPS;
 RZ Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97298311; PubMed=9153759;
 RA Jauniaux J.C., Poirey R.;
 RT "Sequencing analysis of a 36.9 kb fragment of yeast chromosome XV
 reveals 26 open reading frames including SEC63, CDC31, SUG2, GCD1,
 RBL2, PNT1, PAC1 and VPH1".
 RI Yeast 13:483-487(1997).
 RL EMBL: Z75161; CAA99475.1; -.
 DR SGD: S0005779; ARD2.
 DR InterPro: IPR000345; CytC_heme_bind.
 DR InterPro: IPR000182; GCSAcetyltransf.
 DR Pfam: PF00583; Acetyltransf; 1.
 DR PROSITE: PS00190; CYTOCHROME C; 1.
 SQ SEQUENCE 176 AA: 19727 MW: 4F39DC597A690BAC CRC64;

Query Match 31.1% Score 53.5; DB 3; Length 176;
 Best Local Similarity 31.2% Pred. No. 11;
 Matches 10; Conservative 5; Mismatches 14; Indels 3; Gaps 1;

Qy 1 SRAHQSMETPT---DINPANYAGRGIRPVG 29
 Db 120 SECHQNVFVYLPVAVDLTKQWFIAGQFEQVG 151

RESULT 12

Q9RYP2 PRELIMINARY; PRT; 376 AA.
 AC Q9RYP2
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Adenine deaminase-related protein.
 GN DRA0268.
 OS Deinococcus radiodurans.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcaceae;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN (1)
 RC SEQUENCE FROM N.A.
 RZ STRAIN=R1;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Uterback T., Zaleski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RA "genome sequence of the radioresistant bacterium Deinococcus
 radiodurans R1".
 RT Science 286:1571-1577(1999).
 RL EMBL: AE001863; AAF12376.1; -.
 DR TIGR: DRA0268; -.
 KW Complete proteome.
 SQ SEQUENCE 376 AA: 39845 MW: 7AB7FF32F8C45651 CRC64;

Query Match 30.8% Score 53; DB 16; Length 376;
 Best Local Similarity 40.0% Pred. No. 27;
 Matches 12; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 SRAHQSMETPTDINPANYAGRGIRPVGR 30
 Db 177 ARALALAPDVSRPDRHRACGAGGRRRPAQR 206


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RESULT 13
Q8R054
ID Q8R054 PRELIMINARY: PRT: 467 AA.
AC Q8R054
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Similar to sushi-repeat protein.
GN 1110039C07R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxID=10090;
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC028307; AMR02107.1;
DR MGD: MG1:1916042; 1110039C07R1K.
DR InterPro: IPR001128; Cytochrome_P450.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR Pfam: PF02494; HVR; 1.
DR Pfam: PF00084; sushi; 3.
DR SMART: SM00032; CCP; 3.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
SQ SEQUENCE 467 AA; 5309 MW; BB4C01C7E6118BEC CRC64;

Query Match 32.8%; Score 53; DB 11; Length 467;
Best Local Similarity 53.3%; Pred. No. 34;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 13 PDINPAWYAGRGIRP 27
D5 19 PAVTPTWYAGSGYSP 33

RESULT 14
Q8K1F8
ID Q8K1F8 PRELIMINARY: PRT: 468 AA.
AC Q8K1F8
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Sushi-repeat containing protein.
GN 1110039C07R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxID=10090;
RN [2]
RP SEQUENCE FROM N.A.
RA Huang C.-H.; Chen H.; Peng J.; Chen Y.;
RA Huang C.-H.; Chen H.; Peng J.; Chen Y.;
RT "Cloning and characterization of the sushi-repeat containing protein
(RSCP) as a novel interaction partner of Rh type C glycoprotein
(RHCG).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF193640; AAM73691.1;
DR MGD: MG1:1916042; 1110039C07R1K.
DR InterPro: IPR001128; Cytochrome_P450.
DR InterPro: IPR003410; Hvalin.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR Pfam: PF02494; HVR; 1.
DR Pfam: PF00084; sushi; 3.
DR SMART: SM00032; CCP; 3.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
SQ SEQUENCE 468 AA; 53180 MW; 151A952070DC40D4 CRC64;

Query Match 30.8%; Score 53; DB 11; Length 468;
Best Local Similarity 53.3%; Pred. No. 34;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 13 PDINPAWYAGRGIRP 27
D5 19 PAVTPTWYAGSGYSP 33

RESULT 15
Q8U515
ID Q8U515 PRELIMINARY: PRT: 73 AA.
AC Q8U515
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE AGR_L109p.
GN AGR_L109.
OS Agrobacterium tumefaciens (strain C58 / ATCC 31578).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
OX NCBI_taxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RA MESLIN=21608551; PubMed=11743194;
RA Goodner B.; Hinkie G.; Gattung S.; Miller N.; Blanchard M.;
RA Gucillo B.; Goldran B.S.; Cao Y.; Askenazi M.; Hailing C.; Mullin D.;
RA Houmieu K.; Gordon J.; Vaudin M.; Iatchouk O.; Ept A.; Liu F.;
RA Wolam C.; Allinger M.; Doughty D.; Scott C.; Lapkas C.; Varkelz B.;
RA Flanagan C.; Crowell C.; Gursen J.; Lomo C.; Sear C.; Strub G.;
RA Cielo C.; Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
DR EMBL: AE008203; AAK88619.1;
SQ SEQUENCE 73 AA; 8219 MW; 02A6F70FA651F2AB CRC64;

Query Match 30.2%; Score 52; DB 16; Length 73;
Best Local Similarity 47.6%; Pred. No. 6.9;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 3 AHOHSMETPTDINPAWYAGR 23
D5 23 ANTHREDEVRACISVRWLAGR 43

Search completed: November 12, 2003, 11:09:32
Job time : 37 secs

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